

GenCore version 5.1.6
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protein - protein search, using sw model

August 11, 2004, 13:00:42 ; Search time 45.7143 Seconds
(without alignments)
61.807 Million cell updates/sec

-10-661-207-1

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Gapop 10.0 , Gapextent 0.5

checked: 1586107 seqs, 282547505 residues /

number of hits satisfying chosen parameters: 1586107

min DB seq length: 0

WILHELM DE SAD LEGGETH: 2000000

processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

\base : A_Geneseq_29Jan04:*

2: genesep1990s; *
3: ~~genesep1990s~~

4 : [Genealogy2001G1*](#)

366 *Geese and Geese* 2003 as: *

7: geneseqp2003bs:
8: geneseqp2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted.

and is derived by analysis of the total score distribution.

JOURNAL OF CLIMATE

Result	Query ID	Score	Match Length	DB ID	Description
1	4.2	89.4	58	2	Aar78567 BPTI Kuv
2	4.2	89.4	58	2	Aar78568 BPTI Kuv
3	4.2	89.4	58	2	Aar78569 BPTI Kuv
4	4.1	87.2	10	6	Abu09383 Consens
5	4.0	85.1	58	2	Aar99175 Genetic
6	4.0	85.1	58	2	Aar99176 Genetic
7	3.7	78.7	57	2	Aaw47436 Aprotin
8	3.7	78.7	57	2	Aaw47434 Aprotin
9	3.7	78.7	57	2	Aaw47432 Aprotin
10	3.7	78.7	57	2	Aaw47435 Aprotin
11	3.7	78.7	58	2	Aar78552 Human T
12	3.7	78.7	58	2	Aar99184 Genetic
13	3.7	78.7	60	2	Aay08613 Inter-a
14	3.7	78.7	128	2	Aaw82769 Bovine
15	3.7	78.7	128	2	Aaw82766 Bovine
16	3.7	78.7	128	2	Aaw82768 Bovine
17	3.7	78.7	128	2	Aaw82764 Bovine
18	3.7	78.7	128	2	Aaw82771 Bovine
19	3.7	78.7	128	2	Aaw82767 Bovine
20	3.7	78.7	128	2	Aaw82772 Bovine
21	3.7	78.7	129	2	Aaw82765 Bovine
22	3.6	76.6	25	1	Aap91296 Amino a
23	3.6	76.6	56	1	AAP93399 Aprotin
24	3.6	76.6	56	1	Aap93398 Aprotin
25	3.6	76.6	56	1	Aap93397 Aprotin

26	76.6	AAY68060	Kunitz pr
27	76.6	Aau09230	Human KPI
28	76.6	Aap50699	Sequence
29	76.6	Aaw47433	Aprotinin
30	76.6	AAP50700	Sequence
31	76.6	AAP50701	Sequence
32	76.6	AAP50698	Sequence
33	76.6	AAP70336	Sequence
34	76.6	AAP93401	Aprotinin
35	76.6	AAP93400	Aprotinin
36	76.6	AAP92306	Aprotinin
37	76.6	AAP93329	Sequence
38	76.6	AAP93331	Sequence
39	76.6	AAP93330	Sequence
40	76.6	AAR27373	Bovine pa
41	76.6	AAR39801	Kunitz-ty
42	76.6	AAR62524	Pancreati
43	76.6	AAR47179	BPTI . 3/2
44	76.6	AAR78426	Bovine pa
45	76.6	AABR81885	Mature ha

ATTACHMENTS

RESULT 1
AAR78567
ID AAR78567 standard; peptide; 58 AA.
XX
AC AAR78567;
XX
DT 01-MAR-1996 (first entry)
XX
DE BPTI Kunitz domain derivative DPI-7.1.
XX
KW Human; lipoprotein-associated coagulation inhibitor; peptide library;
KW inhibitor; plasmin; bovine; pancreatic trypsin inhibitor; Kunitz domain;
KW

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Misc-difference₁₈ /note= "residue change: Ile to Phe"

WO9518830-A2.
13-JUL-1995.
11-JAN-1995; 95WO-US000298.
11-JAN-1994; 94US-00179658.
10-MAR-1994; 94US-00208265.
(PROT-) PROTEIN ENG CORP.
Markland W, Ladner RC;
WPI; 1995-255042/33.
Novel plasmin inhibiting protein comprising a Kunitz Domain - useful to prevent/treat disorders attributable to excess plasmin activity.
Example 2; Page 36; 59pp; English.
The peptides AAR78435-R78570 are derivatives of the Kunitz domains from a variety of plasmin inhibitors e.g. the human lipoprotein-associated coagulation inhibitor (LACI) Kunitz domains 1, 2 or 3. The peptides were designed based on the Kunitz domains and are named Designed Plasmid Inhibitor (DPI). This peptide is designed based on the bovine pancreatic trypsin inhibitor (BPTI) Kunitz domain (KuDom) (AAR78426). The peptides can be used to prevent or treat a clinical condition exacerbated by plasminogen deficiency or fibrinolysis or fibrinolysis excessive.

CC bleeding associated with thrombolytics
 XX SQ Sequence 58 AA;

Query Match 89.4%; Score 42; DB 2; Length 58;
 Best Local Similarity 70.0%; Pred. No. 1.1;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPCXXXFIRY 10
 Db 12 GPCRARFIRY 21

RESULT 2
 AAR78568 standard; peptide; 58 AA.
 ID AAR78568
 XX AC AAR78568;
 XX DT 01-MAR-1996 (first entry)
 XX DE BPTI Kunitz domain derivative DPI-7.2.
 XX KW Human; lipoprotein-associated coagulation inhibitor; peptide library;
 inhibitor; plasmin; bovine; pancreatic trypsin inhibitor; Kunitz domain;
 fibrinolysis; fibrinogenolysis; bleeding; thrombolytic.
 XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Misc-difference 15 /note= "residue change: Lys to Arg"
 FT Misc-difference 18 /note= "residue change: Ile to Phe"
 FT Misc-difference 39 /note= "residue change: Arg to Gly"
 XX PN WO9518830-A2.
 XX PD 13-JUL-1995.
 XX PF 11-JAN-1995; 95WO-US000298.
 XX PR 11-JAN-1994; 94US-00179658.
 XX PR 10-MAR-1994; 94US-00208265.
 XX PA (PROT-) PROTEIN ENG CORP.
 XX PI Markland W, Ladner RC;
 XX DR WPI; 1995-255042/33.
 XX PT Novel Plasmin inhibiting protein comprising a Kunitz Domain - useful to prevent/treat disorders attributable to excess plasmin activity.
 XX PS Example 2; Page 36; 59pp; English.
 XX CC The peptides AAR78435-R78570 are derivatives of the Kunitz domains from a variety of plasmin inhibitors e.g. the human lipoprotein-associated coagulation inhibitor (LACI) Kunitz domains 1, 2 or 3. The peptides were designed based on the Kunitz domains and are named Designed Plasmid Inhibitor (DPI). This peptide is designed based on the bovine pancreatic trypsin inhibitor (BPTI) Kunitz domain (KuDom) (AAR78426). The peptides can be used to prevent or treat a clinical condition exacerbated by plasmin e.g. inappropriate fibrinolysis or fibrinogenolysis, excessive bleeding associated with thrombolytics

XX SQ Sequence 58 AA;

Query Match 89.4%; Score 42; DB 2; Length 58;
 Best Local Similarity 70.0%; Pred. No. 1.1;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPCXXXFIRY 10
 Db 12 GPCRARFIRY 21

RESULT 4
 ABU09383
 ID ABU09383 standard; peptide; 10 AA.
 XX AC ABU09383;

17-JUL-2003 (first entry)

Consensus peptide sequence for mammalian Kunitz inhibitor.

Protein purification; protein isolation; recombinant fusion polypeptide; enzyme/tagged-peptide binding; fusion protein; tag peptide; recombinant capture protein; mammalian; Kunitz inhibitor.

Mammalia.
Synthetic.

Key Location/Qualifiers

Misc-difference 4 /label= Lys, Arg

Misc-difference 5 /label= GLY, Ala

Misc-difference 6 /label= Arg, Gly, Ser

EP1281716-A2.

05-FEB-2003.

06-JUL-2002; 2002EP-00015128.

10-JUL-2001; 2001US-00901996.

(HOFF) ROCHE DIAGNOSTICS GMBH.

(HOFF) HOFFMANN LA ROCHE & CO AG F.

Dwulet FE, Balgobin NG, McCarthy RC;

WPI; 2003-334999/32.

Purifying or isolating a recombinant fusion peptide, comprises forming a fusion peptide comprising a tag peptide covalently attached to a polypeptide and contacting the fusion peptide with an enzyme or modified enzyme.

Claim 9; Page 6; 17pp; English.

The present invention relates to a method for purifying or isolating a recombinant fusion polypeptide based on enzyme/tagged-peptide binding. The method comprises forming a fusion protein comprising a tag peptide sequence covalently attached to a polypeptide sequence, and contacting the fusion peptide with an enzyme or modified enzyme that specifically binds to the tag peptide sequence to form a complex between the enzyme or modified enzyme and the fusion peptide. The method of the invention is useful for purifying or isolating recombinant fusion polypeptides. The present method of using enzymes as capture agents offers several advantages not currently found in prior art. For example (a) it is possible to select natural or recombinant capture proteins with modified binding sites that will have different affinities for the same tag, (b) it is possible to modify the amino acid sequence of the tag to generate high, medium and low affinity peptide tags for use in different applications with the same capture protein, and (c) depending upon the application, natural or recombinant capture proteins with increased or decreased resistance to denaturation can also be prepared. Such versatility is amenable to the development of a variety of standardised binding and elution conditions for the isolation of tagged proteins or their complexes. ABU09383-ABU09395 represent peptides that may be used as tag peptides in the method of the present invention

Sequence 10 AA;

Query Match 87.2%; Score 41; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GPCXXXFIRY 10
1 GPCXXXFIRY 10

RESULT 5
AAR99175
ID AAR99175 standard; protein; 58 AA.
XX
AC AAR99175;
XX
DT 12-FEB-1997 (First entry)

DE Genetically engineered aprotinin-like Kunitz domain (DPI.2.2).
XX
KW Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
KW alaphal antitrypsin; respiratory disorder; cystic fibrosis;
KW smokers emphysema.
XX
OS Synthetic.
XX
PN WO9620278-A2.
XX
PD 04-JUL-1996.
XX
PP 15-DEC-1995; 95WO-US016349.
XX
PR 16-DEC-1994; 94US-00358160.
XX
PA (PROT-) PROTEIN ENG CORP.
XX
PI Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;
XX
WPI; 1996-321851/32.
XX
PT New engineered inhibitors of human neutrophil elastase - contg. aprotinin
PT -like Kunitz domain for treating, e.g. cystic fibrosis or other
PT respiratory disorders.
XX
PS Claim 1; Page 50; 105pp; English.

CC Genetically engineered human derived Kunitz domains can be used to
CC inhibit human neutrophil elastase, an enzyme involved in the elimination
CC of pathogens and the restructuring of connective tissue. In cases of
CC reduction of the circulating alpha-1-protease inhibitor (API or alpha1
CC antitrypsin), or the inactivation of API by oxidation (smokers
CC emphysema), extensive destruction of the lung tissue may result from
CC uncontrollable elastolytic activity of human neutrophil elastase. Other
CC respiratory disorders such as cystic fibrosis are thought to be caused by
CC human neutrophil elastase release by neutrophils. The genetically
CC engineered human derived Kunitz domains can be used to treat such
CC respiratory disorders. See AAR99146-R99211
XX
SQ Sequence 58 AA;

Query Match 85.1%; Score 40; DB 2; Length 58;
Best Local Similarity 60.0%; Pred. No. 2.7;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GPCXXXFIRY 10

DB 12 GPCIALFLRY 21

RESULT 6

AAR99176
ID AAR99176 standard; protein; 58 AA.
XX
AC AAR99176;
XX
DT 12-FEB-1997 (First entry)
XX
DE Genetically engineered aprotinin-like Kunitz domain (DPI.2.3).
XX
KW Aprotinin; Kunitz domain; human neutrophil elastase; hNE;

connective tissue; alpha 1 protease inhibitor; API; neutrophil; alaphal antitrypsin; respiratory disorder; cystic fibrosis; smokers emphysema. Synthetic.

XX OS WO9620278-A2.
 XX PN 04-JUL-1996.
 XX PD 15-DEC-1995; 95WO-US016349.
 XX PR 16-DEC-1994; 94US-00358160.
 XX PA (PROT-) PROTEIN ENG CORP.
 XX PI Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;
 XX DR WPI; 1996-321851/32.

XX PT New engineered inhibitors of human neutrophil elastase - contg. aprotinin -like Kunitz domain for treating, e.g. cystic fibrosis or other respiratory disorders.

XX PS Claim 1; Page 50; 105pp; English.

XX CC Genetically engineered human derived Kunitz domains can be used to inhibit human neutrophil elastase, an enzyme involved in the elimination of pathogens and the restructuring of connective tissue. In cases of reduction of the circulating alpha-1-protease inhibitor (API or alpha1 antitrypsin), or the inactivation of API by oxidation (smokers emphysema), extensive destruction of the lung tissue may result from uncontrolled elastolytic activity of human neutrophil elastase. Other respiratory disorders such as cystic fibrosis are thought to be caused by human neutrophil elastase release by neutrophils. The genetically engineered human derived Kunitz domains can be used to treat such respiratory disorders. See AAR99146-R99211

XX SQ Sequence 58 AA;

Query Match 85.1%; Score 40; DB 2; Length 58;
 Best Local Similarity 60.0%; Pred. No. 2.7;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPCXXXFIRY 10
 Db 12 GPCIAFFIRY 21

RESULT 7
 AAW47436 ID AAW47436 standard; peptide; 57 AA.
 XX AC AAW47436;
 XX DT 26-JUN-1998 (First entry)
 XX DE Aprotinin variant 3.
 XX KW Aprotinin variant; serine protease inhibitor.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN EP821007-A2;
 XX PD 28-JAN-1998.
 XX PF 14-JUL-1997; 97EP-00111980.
 XX PR 25-JUL-1996; 96DE-01029982.
 XX PA {FARB } BAYER AG.
 XX PI Schroeder W, Bjorn S, Norris K, Dines V, Norkskov-Lauritsen L;
 XX PI Christensen ND;
 XX DR WPI; 1998-102619/10.

XX OS Aprotinin variants Prepared by recombinant DNA techniques - useful as PT protease inhibitors in surgery and medicine.

XX PS Claim 5; Fig 1; 19pp; German.

XX CC The present sequence is an aprotinin variant, which can be used as a serine protease inhibitor, e.g. in surgery to reduce blood loss, to treat multiple trauma, shock, pain, oedema, stroke and inflammation and to inhibit invasive tumour growth and metastasis, inflammation, coagulation and risk of haemorrhage in dialysis therapy and artificial organs.
 CC Compared with wild type aprotinin, the variant is less reactive with anti-aprotinin antibodies, less immunogenic, causes less histamine release from blood cells, exhibits reduced renal accumulation and has improved Ki values

XX SQ Sequence 57 AA;

Query Match 78.7%; Score 37; DB 2; Length 57;
 Best Local Similarity 60.0%; Pred. No. 9.8;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps

Qy 1 GPCXXXFIRY 10
 Db 11 GPCRASIRY 20

RESULT 8
 AAW47434 ID AAW47434 standard; peptide; 57 AA.
 XX AC AAW47434;
 XX DT 26-JUN-1998 (first entry)
 XX DE Aprotinin variant 3.
 XX KW Aprotinin variant; serine protease inhibitor.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN EP821007-A2;
 XX PD 28-JAN-1998.
 XX PF 14-JUL-1997; 97EP-00111980.
 XX PR 25-JUL-1996; 96DE-01029982.
 XX PA {FARB } BAYER AG.
 XX PI Schroeder W, Bjorn S, Norris K, Dines V, Norkskov-Lauritsen L;
 XX PI Christensen ND;
 XX DR WPI; 1998-102619/10.

XX OS Aprotinin variants Prepared by recombinant DNA techniques - useful as PT protease inhibitors in surgery and medicine.

XX PS Claim 5; Fig 1; 19pp; German.

XX CC The present sequence is an aprotinin variant, which can be used as a serine protease inhibitor, e.g. in surgery to reduce blood loss, to treat multiple trauma, shock, pain, oedema, stroke and inflammation and to inhibit invasive tumour growth and metastasis, inflammation, coagulation and risk of haemorrhage in dialysis therapy and artificial organs.
 CC Compared with wild type aprotinin, the variant is less reactive with anti-aprotinin antibodies, less immunogenic, causes less histamine release from blood cells, exhibits reduced renal accumulation and has improved Ki values

XX PD 28-JAN-1998.
 XX PF 14-JUL-1997; 97EP-00111980.
 XX PR 25-JUL-1996; 96DE-01029982.
 XX PA {FARB } BAYER AG.

treatment of Alzheimer's disease.
Disclosure; Fig 8B; 72pp; English.

This invention describes novel transgenic mice expressing proteins related to the pathology of Alzheimer's disease and which provide models for studying potentially therapeutic compounds. The transgenic mice contain a DNA sequence encoding a beta-amyloid precursor protein (APP) and a nerve tissue specific promoter operably linked to the beta-APP allowing its expression to form beta-amyloid protein deposits in the animal's brain. The transgenic mouse is useful for elucidating the molecular mechanisms involved in the synthesis of and, more importantly, inhibiting the synthesis and deposition of beta-amyloid proteins (most importantly in the brain where plaque formation is associated with Alzheimer's disease) by inhibiting production and/or increasing cleavage after production. The transgenic animals provide useful models for studying the in vivo relationships of the proteins to each other and to other compounds being tested for their usefulness in treating Alzheimer's disease.

Sequence 60 AA;

Query Match 78.7%; Score 37; DB 2; Length 60;

Matches 6; Local Similarity 60.0%; Pred. No. 10;
Indels 0; Gaps 0; Mismatches 0;

1 GPCXXXFIRY 10

14 GPCRAAMIRY 23

Query Match 78.7%; Score 37; DB 2; Length 128;

Matches 6; Local Similarity 60.0%; Pred. No. 20;
Indels 4; Gaps 0; Mismatches 0;

QY 1 GPCXXXFIRY 10

DB 82 GPCRAAMIRY 91

Sequence 128 AA;

Aprotinin; bovine; pancreatic trypsin inhibitor; BPTI; variant; bikinin; inhibitor; kallikrein; plasmin; factor Xa; elastase; blood loss; shock; thromboembolic disorder; polytrauma; sepsis; coagulation; organ failure; angina; myocardial infarct; stroke; embolism; thrombosis; restenosis; perfusion injury, inflammatory disorder; tumour invasion; metastasis; pain; oedema; haemostasis; dialysis.

Bos taurus.

Synthetic.

DE19725014-A1.

17-DEC-1998.

13-JUN-1997; 97DE-01025014.

(FARB) BAYER AG.

Schroeder W, Apeler H;

PI XX

PR 13-JUN-1997; 97DE-01025014.

WPI; 1999-046858/05.

Ne aprotinin and bikinin variants - useful for reducing blood loss during surgery, for treating e.g. thromboembolic disorders.

Disclosure; Fig 2; 40pp; German.

Schroeder W, Apeler H;

WPI; 1999-046858/05.

Ne aprotinin and bikinin variants - useful for reducing blood loss during surgery, for treating e.g. thromboembolic disorders.

Disclosure; Fig 2; 40pp; German.

AAW82763-W82772 represent variants of the bovine bikinin peptide which is composed of two aprotinin (also known as bovine pancreatic trypsin inhibitor, BPTI) that have a net charge of +3 to -3 at pH 7. The bikunins are kallikrein, plasmin, factor Xa inhibitors. The bikunins are kallikrein, plasmin, factor Xa and elastase inhibitors. The aprotinins and bikunins can be used to reduce blood loss during surgery, to treat thromboembolic disorders, shock, polytrauma, sepsis, disseminated intravasal coagulation, multi-organ failure, unstable angina, myocardial infarct, stroke, embolism, deep vein thrombosis, restenosis, perfusion injury, thrombosis and bleeding after thrombosis, to treat inflammatory disorders, to inhibit tumour invasion and

aprotinins are kallikrein, plasmin and factor Xa inhibitors. The bikunins are kallikrein, plasmin, factor Xa and elastase inhibitors. The aprotinins and bikunins can be used to reduce blood loss during surgery, to treat thromboembolic disorders, shock, polytrauma, sepsis, disseminated intravasal coagulation, multi-organ failure, unstable angina, myocardial infarct, stroke, embolism, deep vein thrombosis, restenosis, perfusion injury, thrombosis and bleeding after thrombosis, to treat inflammatory disorders, to inhibit tumour invasion and

CC aprotinins are kallikrein, plasmin, factor Xa and elastase inhibitors. The CC bikunins are kallikrein, plasmin, factor Xa and elastase inhibitors. The CC aprotinins and bikunins can be used to reduce blood loss during surgery,

CC to treat thromboembolic disorders, shock, polytrauma, sepsis, disseminated intravasal coagulation, multi-organ failure, unstable angina, myocardial infarct, stroke, embolism, deep vein thrombosis, restenosis, perfusion injury, thrombosis and bleeding after thrombosis,

CC to treat inflammatory disorders, to inhibit tumour invasion and

CC activation, during dialysis. The variants have altered or enhanced

CC protease inhibition specificities

XX SQ Sequence 128 AA;

Query Match 78.7%; Score 37; DB 2; Length 128;

Best Local Similarity 60.0%; Pred. No. 20;

Matches 6; Conservative 0; MisMatches 0; Indels 4; Gaps 0;

QY 1 GPCXXXFIRY 10

DB 82 GPCRAAMIRY 91

Sequence 128 AA;

RESULT 15

AAW82766

ID AAW82766 standard; peptide; 128 AA.

XX

AC AAW82766;

XX

22-APR-1999 (first entry)

DT XX

Bovine bikinin peptide, variant #3.

DE XX

Aprotinin; bovine; pancreatic trypsin inhibitor; BPTI; variant; bikinin;

KW inhibitor; kallikrein; plasmin; factor Xa; elastase; blood loss; shock;

KW thromboembolic disorder; polytrauma; sepsis; coagulation; organ failure;

KW angina; myocardial infarct; stroke; embolism; thrombosis; restenosis;

KW perfusion injury, inflammatory disorder; tumour invasion; metastasis;

KW pain; oedema; haemostasis; dialysis.

XX Bos taurus.

OS Synthetic.

XX PN DE19725014-A1.

XX PD 17-DEC-1998.

XX PF 13-JUN-1997; 97DE-01025014.

XX PR 13-JUN-1997; 97DE-01025014.

XX PA (FARB) BAYER AG.

XX PI Schroeder W, Apeler H;

XX DR 13-JUN-1997; 97DE-01025014.

XX PT WPI; 1999-046858/05.

XX Ne aprotinin and bikinin variants - useful for reducing blood loss during

XX surgery, for treating e.g. thromboembolic disorders.

XX Disclosure; Fig 2; 40pp; German.

XX AAW82764-W82772 represent variants of the bovine bikinin peptide which is

CC composed of two aprotinin (also known as bovine pancreatic trypsin

CC inhibitor, BPTI) that have a net charge of +3 to -3 at pH 7. The

CC bikunins are kallikrein, plasmin, factor Xa inhibitors. The bikunins

are kallikrein, plasmin, factor Xa and elastase inhibitors. The

aprotinins and bikunins can be used to reduce blood loss during

CC surgery, to treat thromboembolic disorders, shock, polytrauma, sepsis,

CC activation, during dialysis. The variants have altered or enhanced

CC protease inhibition specificities

XX SQ Sequence 128 AA;

Query Match 78.7%; Score 37; DB 2; Length 128;

Best Local Similarity 60.0%; Pred. No. 20;

Matches 6; Conservative 0; MisMatches 0; Indels 4; Gaps 0;

QY 1 GPCXXXFIRY 10

DB 82 GPCRAAMIRY 91

Sequence 128 AA;

RESULT 15

AAW82766

ID AAW82766 standard; peptide; 128 AA.

XX

AC AAW82766;

XX

22-APR-1999 (first entry)

DT XX

Bovine bikinin peptide, variant #3.

DE XX

Aprotinin; bovine; pancreatic trypsin inhibitor; BPTI; variant; bikinin;

KW inhibitor; kallikrein; plasmin; factor Xa; elastase; blood loss; shock;

KW thromboembolic disorder; polytrauma; sepsis; coagulation; organ failure;

KW angina; myocardial infarct; stroke; embolism; thrombosis; restenosis;

KW perfusion injury, inflammatory disorder; tumour invasion; metastasis;

KW pain; oedema; haemostasis; dialysis.

XX Bos taurus.

OS Synthetic.

XX PN DE19725014-A1.

XX PD 17-DEC-1998.

XX PF 13-JUN-1997; 97DE-01025014.

XX PR 13-JUN-1997; 97DE-01025014.

XX DR 13-JUN-1997; 97DE-01025014.

XX PT WPI; 1999-046858/05.

XX Ne aprotinin and bikinin variants - useful for reducing blood loss during

XX surgery, for treating e.g. thromboembolic disorders.

XX Disclosure; Fig 2; 40pp; German.

XX AAW82763-W82772 represent variants of the bovine bikinin peptide which is

CC composed of two aprotinin (also known as bovine pancreatic trypsin

CC inhibitor, BPTI) that have a net charge of +3 to -3 at pH 7. The

CC bikunins are kallikrein, plasmin, factor Xa inhibitors. The bikunins

are kallikrein, plasmin, factor Xa and elastase inhibitors. The

aprotinins and bikunins can be used to reduce blood loss during

CC surgery, to treat thromboembolic disorders, shock, polytrauma, sepsis,

CC activation, during dialysis. The variants have altered or enhanced

CC protease inhibition specificities

CC metastasis, to treat pain and oedema and to inhibit haemostasis
CC activation during dialysis. The variants have altered or enhanced
CC protease inhibition specificities

SQ	Sequence 128 AA;						
Qy	1 GPCXXXFIRY .10						
Query Match	78.7%	Score 37;	DB 2;	Length 128;			
Best Local Similarity	60.0%	Pred. No.	20;				
Matches	6;	Mismatches	0;	Indels	0;	Gaps	0;
	Conservative						

Search completed: August 11, 2004, 13:07:39
Job time : 46.7143 secs

GenCore version 5.1.6
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rotein - protein search, using sw model

on: August 11, 2004, 13:04:58 ; Search time 10.9524 Seconds
 (without alignments)
 87.827 Million cell updates/sec

e: US-10-661-207-1
 ect score: 47
 ence: 1 GPCXXXFIRY 10

ing table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

ched: 283366 seqs, 96191526 residues

i1 number of hits satisfying chosen parameters: 283366

.num DB seq length: 0
 .num DB seq length: 200000000

-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

base : PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

1 number of hits satisfying chosen parameters:

283366

Processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

base : PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

#	Query	Match	Length	DB	ID	Description
1	42	89.4	122	1	A55115	uterine plasmin/trypsin inhibitor - pig
2	39	83.0	57	2	A59204	C;Species: Sus scrofa domesticus (domestic pig)
3	37	78.7	60	1	TIBOR	C;Date: 10-Sep-1999 #sequence_change 10-Sep-1999
4	36	76.6	58	2	S10063	C;Accession: A55115
5	36	76.6	59	2	S00371	R;Stallings-Mann, M.L.; Burke, M.G.; Trout, W.E.; Roberts, R.M.
6	36	76.6	100	1	TIBO	J. Biol. Chem. 269, 24090-24094, 1994
7	36	76.6	100	1	TIBOSP	A;Title: Purification, characterization, and cDNA cloning of a Kunitz-type proteinase inhibitor
8	35	74.5	61	1	THCBP	A;Reference number: A55115; MUID:95014140; PMID:7929061
9	35	74.5	62	2	S07451	A;Status: preliminary
10	35	74.5	67	1	TIBOC	A;Molecule type: mRNA
11	35	74.5	324	2	AB0767	A;Cross-references: GB:L114282; NID:9682652; PID:9682653
12	35	74.5	330	1	S15303	A;Note: authors translated the codon GGC for residue 36 as Ala, AGC for residue 48 as Arg
13	35	74.5	580	2	T20716	C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
14	35	74.5	2225	2	T26063	C;Keywords: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
15	34	72.3	91	2	I68704	F;38-88/Domain: basic proteinase inhibitor homolog
16	34	72.3	123	2	A29652	F;38-88/Domain: basic proteinase inhibitor homolog
17	34	72.3	235	2	A54951	F;38-88/Domain: basic proteinase inhibitor homolog
18	34	72.3	250	2	I48850	F;38-88/Domain: basic proteinase inhibitor homolog
19	34	72.3	352	1	TIBOBI	F;38-88/Domain: basic proteinase inhibitor homolog
20	34	72.3	361	2	B25132	F;38-88/Domain: basic proteinase inhibitor homolog
21	34	72.3	361	2	I48851	F;38-88/Domain: basic proteinase inhibitor homolog
22	34	72.3	372	2	A25148	F;38-88/Domain: basic proteinase inhibitor homolog
23	34	72.3	384	2	A25132	F;38-88/Domain: basic proteinase inhibitor homolog
24	34	72.3	384	2	I54499	F;38-88/Domain: basic proteinase inhibitor homolog
25	33	70.2	30	2	S07484	F;38-88/Domain: basic proteinase inhibitor homolog
26	33	70.2	53	2	B29235	F;38-88/Domain: basic proteinase inhibitor homolog
27	33	70.2	1553	2	T09361	F;38-88/Domain: basic proteinase inhibitor homolog
28	32	68.1	56	2	JND380	F;38-88/Domain: basic proteinase inhibitor homolog
29	32	68.1	58	1	TIHABK	F;38-88/Domain: basic proteinase inhibitor homolog

RESULT 1
 A55115
 uterine plasmin/trypsin inhibitor - pig
 C;Species: Sus scrofa domesticus (domestic pig)
 C;Date: 10-Sep-1999 #sequence_change 10-Sep-1999
 C;Accession: A55115
 R;Stallings-Mann, M.L.; Burke, M.G.; Trout, W.E.; Roberts, R.M.
 J. Biol. Chem. 269, 24090-24094, 1994
 A;Title: Purification, characterization, and cDNA cloning of a Kunitz-type proteinase inhibitor
 A;Reference number: A55115; MUID:95014140; PMID:7929061
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-122 <STA>
 A;Cross-references: GB:L114282; NID:9682652; PID:9682653
 A;Note: authors translated the codon GGC for residue 36 as Ala, AGC for residue 48 as Arg
 C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
 C;Keywords: serine proteinase inhibitor
 F;38-88/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 Query Match 1 GPCXXXFIRY 10
 Best Local Similarity 89.4%; Score 42;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY ||||| :|||
 Db 45 GPCSAHFVRY 54
 RESULT 2
 A59204
 basic proteinase inhibitor - great pond snail
 N;Alternate names: trypsin inhibitor
 C;Species: Lymnaea stagnalis (great pond snail)
 C;Date: 04-Mar-2000 #sequence_change 04-Mar-2000
 C;Accession: A59204
 R;Nagle, G.
 submitted to the Protein Sequence Database, March 2000
 A;Description: Lymnaea trypsin inhibitor.
 A;Reference number: A59204
 A;Accession: A59204
 A;Molecule type: protein
 A;Residues: 1-57 <NAG>
 A;Experimental source: albumen gland
 C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
 C;Keywords: glycoprotein; serine proteinase inhibitor
 F;5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 F;5-55,14-38,30-51/Disulfide bonds: #status predicted
 F;15/Inhibitory site: Lys (trypsin) #status predicted
 F;24/Binding site: carbohydrate (Asn) (covalent) #status experimental
 Query Match 83.0%; Score 39; DB 2; Length 57;

Best Local Similarity 60.0%; **Pred. No.** 0.16;
Matches 6; **Conservative** 1; **Mismatches** 3; **Indels** 0; **Gaps** 0;

Qy 1 GPCXXXFIRY 10
 | | | | : |
 Db 12 GPCKGNFLRY 21

RESULT 3

TIBOR
 serum basic proteinase inhibitor - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 31-Oct-1980 #sequence_revision 31-Oct-1980 #text_change 31-Dec-1993
 C;Accession: A01206
 R;Wachter, E.; Deppner, K.; Hochstrasser, K.; Lempert, K.; Geiger, R.
 FEBS Lett. 119, 58-62, 1980
 A;Title: A new Kunitz-type inhibitor from bovine serum amino acid sequence determination
 A;Reference number: A01206; MUID:8104440B; PMID:7428928
 A;Accession: A01206
 A;Molecule type: protein
 A;Residues: 1-60 <WAC>
 C;Comment: This inhibitor has activity very similar to that of the basic protease inhibitor homolog
 C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
 C;Keywords: serine proteinase inhibitor
 F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 F;17/Inhibitory site: Lys (trypsin) #status experimental

Query Match 78.7%; Score 37; DB 1; Length 60;
 Best Local Similarity 60.0%; Pred. No. 0.46;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GPCXXXFIRY 10
 | | | | : |
 Db 14 GPCKAAMIRY 23

RESULT 4

S10063
 isoaprotinin G2 - bovine hybrid
 C;Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 13-Jun-1997
 C;Accession: S10063
 R;Siekmann, J.; Wenzel, H.R.; Schroeder, W.; Tschesche, H.
 Biol. Chem. Hoppe-Seyler 369, 157-163, 1988
 A;Title: Characterization and sequence determination of six aprotinin homologues from bovine
 A;Reference number: S00371; MUID:88221840; PMID:2453200
 A;Accession: S10063
 A;Molecule type: protein
 A;Residues: 1-58 <SIE>
 C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
 C;Keywords: serine proteinase inhibitor
 F;5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 F;15/Inhibitory site: Lys (trypsin) #status predicted

Query Match 76.6%; Score 36; DB 2; Length 58;
 Best Local Similarity 60.0%; Pred. No. 0.73;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GPCXXXFIRY 10
 | | | | : |
 Db 12 GPCKARMIRY 21

RESULT 5

S00371
 isoaprotinin G1 - bovine hybrid
 C;Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 13-Jun-1997
 C;Accession: S00371
 R;Siekmann, J.; Wenzel, H.R.; Schroeder, W.; Tschesche, H.
 Biol. Chem. Hoppe-Seyler 369, 157-163, 1988
 A;Title: Characterization and sequence determination of six aprotinin homologues from bovine
 A;Reference number: S00371; MUID:88221840; PMID:2453200

:ference number: A92023; MUID:66171231; PMID:5296424
 :ntents: annotation; disulfide bonds
 :cession: A92023
 :olecule type: protein
 :sidues: 36-93 <AN2>
 lauvet, J.; Achter, R.
 : Soc. Chim. Biol. 49, 985-1000, 1967
 :title: La structure covalente d'un inhibiteur polypeptidique de la trypsin (inhibiteur
 :ference number: A90736; MUID:68012003; PMID:6053284
 :ntents: annotation; disulfide bonds
 :cession: A90736
 :olecule type: protein
 :sidues: 36-93 <DLQ>
 uber, R.; Kukla, D.; Ruhmann, A.; Epp, O.; Formanek, H.
 urwissenschaften 57, 389-392, 1970
 title: The basic trypsin inhibitor of bovine pancreas. I. Structure analysis and config
 :ference number: A93410; MUID:70255230; PMID:5447861
 :ntents: annotation; X-ray crystallography of basic protease inhibitor, 2.5 angstrom
 :wig, R.V.; Ray, P.; Coguill, R.; Krugel, W.
 hem. Biophys. Res. Commun. 167, 543-547, 1990
 :title: Presence of pancreatic trypsin inhibitor in adrenal medullary chromaffin cells.
 :ference number: A34658; MUID:90211226; PMID:2322242
 :cession: A34658
 :de Anderson, S.; Kingston, I.B.
 : Natl. Acad. Sci. U.S.A. 80, 6838-6842, 1983
 :title: Isolation of a genomic clone for bovine pancreatic trypsin inhibitor by using a
 :ference number: A93977; MUID:84070725; PMID:6580617
 :cession: A93977
 :olecule type: protein
 :sidues: 'PSLFNRDPPIPA', '34-97,' 'GKIGGRAGEEGKG', '<AND>
 os-s-references: GB:X03365; GB:K00966; MID:91364183
 emann, J.; Wenzel, H.R.; Schroeder, W.; Tschesche, H.
 : Chem. Hoppe-Seyler 369, 157-163, 1988
 :title: Characterization and sequence determination of six aprotinin homologues from bo
 :ference number: S00371; MUID:88221840; PMID:2453200
 :cession: S10062
 :olecule type: protein
 :sidues: 36-66, 'P', 68-82, 'S', 84-93 <SIE>
 :periment source: lung
 :mmemt: Basic proteinase inhibitor is an intracellular polypeptide found in many tissue
 :metrics: 34/1; 98/1
 :perfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
 :ywords: serine proteinase inhibitor
 :20/Domain: signal sequence #status predicted <SIG>
 :35/Domain: propeptide #status predicted <PRO>
 :1-100/Product: basic proteinase inhibitor #status experimental <MAT>
 :1-90/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 :1-90,49-73,65-86/Disulfide bonds: #status experimental
 /Inhibitory site: Lys (trypsin, chymotrypsin, kallikrein, plasmin) #status experiment
 :ery Match 76.6%; Score 36; DB 1; Length 100;
 :st Local Similarity 60.0%; Pred. No. 1.2;
 itches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 1 GPCXXXFIRY 10
 47 GPCKARIIRY 56
 :en basic proteinase inhibitor precursor - bovine

N;Alternate names: isoaprotinin 1
 :Species: Bos primigenius taurus (cattle)
 C;Date: 07-Sep-1990 #text revision 22-Jul-1994 #text Change 21-Jul-2000
 C;Accession: S00274; B30333; A27417; S10547; S13478; A23915; S10064
 R;Creighton, T.E.; Charles, I.G.
 J. Mol. Biol. 194, 11-22, 1987
 A;Title: Sequences of the genes and polypeptide precursors for two bovine protease inhibitor,
 A;Reference number: S00274; MUID:87283904; PMID:2441071
 A;Accession: S00274
 A;Molecule type: mRNA
 A;Residues: 1-100 <CR2>
 A;Cross-references: EMBL:X05275; PIDN:AAA51418.1; PID:9163720
 R;Barra, D.; Simmaco, M.; Bossa, F.; Fioretti, E.; Angeletti, M.; Ascoli, F.
 Cold Spring Harb. Symp. Quant. Biol. 52, 511-519, 1987
 A;Title: Biosynthesis, processing, and evolution of bovine pancreatic trypsin inhibitor.
 A;Reference number: A90926; MUID:88295740; PMID:2456884
 A;Accession: B30333
 A;Molecule type: DNA
 A;Residues: 1-100 <CRE>
 A;Cross-references: GB:M20935; GB:X05275; NID:9163718; PIDN:AAA51418.1; PID:9163720
 R;Barra, D.; Simmaco, M.; Bossa, F.; Fioretti, E.; Angeletti, M.; Ascoli, F.
 J. Biol. Chem. 262, 13916-13919, 1987
 A;Title: Primary structure of a protease isoform inhibitor from bovine spleen. A possible inte
 A;Reference number: A27417; MUID:88007630; PMID:3654647
 A;Accession: A27417
 A;Molecule type: protein
 A;Residues: 34-99 <BAR>
 A;Note: the more abundant form of isoform inhibitor I lacks 99-Asn
 R;Fioretti, E.; Angeletti, M.; Fiorucci, L.; Barra, D.; Bossa, F.; Ascoli, F.
 Biol. Chem. Hoppe-Seyler 369(Suppl.), 37-42, 1988
 A;Title: Primary structure of isoform inhibitors in bovine organs.
 A;Reference number: S02485; MUID:89076531; PMID:2462435
 A;Accession: S02487
 A;Molecule type: protein
 A;Residues: 34-99 <FIO>
 R;Kingston, I.B.; Anderson, S.
 Biochem. J. 233, 443-450, 1986
 A;Title: Sequences encoding two trypsin inhibitors occur in strikingly similar genomic er
 A;Reference number: S10546; MUID:86158754; PMID:2420326
 A;Accession: S10547
 A;Molecule type: DNA
 A;Residues: 34-97 <KIN>
 R;Barra, D.; Fioretti, E.; Angeletti, M.; Maras, B.; Bossa, F.; Ascoli, F.
 Biochim. Biophys. Acta 1076, 143-147, 1991
 A;Title: Proteinase isoform inhibitors from bovine spleen: primary structure of an intermediat
 A;Reference number: S13478; MUID:91098258; PMID:1986787
 A;Accession: S13478
 A;Molecule type: protein
 A;Residues: 36-97 <BA2>
 R;Fioretti, E.; Iacopino, G.; Angeletti, M.; Barra, D.; Bossa, F.; Ascoli, F.
 J. Biol. Chem. 260, 11451-11455, 1985
 A;Reference number: A23915; MUID:86008178; PMID:2413011
 A;Accession: A23915
 A;Molecule type: protein
 A;Residues: 36-93 <FI2>
 A;Note: three disulfide bonds are present
 R;Siekmann, J.; Wenzel, H.R.; Schroeder, W.; Tschesche, H.
 Biol. Chem. Hoppe-Seyler 369, 157-163, 1988
 A;Title: Characterization and sequence determination of six aprotinin homologues from bo
 A;Reference number: S00371; MUID:88221840; PMID:2453200
 A;Accession: S10064
 A;Molecule type: protein
 A;Residues: 36-93 <SIE>
 A;Experimental source: lung
 C;Comment: This inhibitor is found in many bovine organs. In spleen, it is located in vas
 C;Comment: Compared with the basic proteinase inhibitor, affinity for trypsin and chymot
 C;Genetics: Inhibitors I and III are intermediates in the processing of the precursor to t
 A;Introns: 34/1; 98/1
 C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
 C;Keywords: serine proteinase inhibitor
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-33/Domain: propeptide #status predicted <PRO>

tches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 1 GPCXXXFIR 9
 184 GPGTFF FIR 192

LT 12
 03 CDP-5-deoxy-Delta(3,4)-glucosene reductase (EC 1.3.1.-) - *Salmonella typhimurium*
 alternate names: hypothetical protein 7.6
 species: *Salmonella typhimurium*
 date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 session: S15303
 ang, X.M.; Neal, B.; Santiago, F.; Lee, S.J.; Romana, L.K.; Reeves, P.R.
 Microbiol. 5, 695-713, 1991
 title: Structure and sequence of the rfb (O antigen) gene cluster of *Salmonella serovar*
 reference number: S15296; PMID:91260454; MUID:1710759
 session: S15303
 status: preliminary
 molecule type: DNA
 residues: 1-330 <MOL>
 superfamily: methane monooxygenase reductase component; cytochrome-b5 reductase homolog
 keywords: 2Fe-2S; iron-sulfur protein; metalloprotein; oxidoreductase
 -72/Domain: ferredoxin [2Fe-2S] homology <FER>
 1-320/Domain: cytochrome-b5 reductase homology <CBR>
 ,42,45,71/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted
 Query Match 74.5%; Score 35; DB 1; Length 330;
 best Local Similarity 66.7%; Pred. No. 5.4;
 tches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 1 GPCXXXFIR 9
 184 GPGTFF FIR 192

LT 13
 03 hypothetical protein F10F2.8 - *Caenorhabditis elegans*
 species: *Caenorhabditis elegans*
 date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 session: T20716
 les, L.
 vited to the EMBL Data Library, August 1994
 reference number: Z19313
 1580 <WIL>
 atus: preliminary; translated from GB/EMBL/DDBJ
 molecule type: DNA
 residues: EMBL:Z35598; PIDN:CAA84654.1; GSPDB:GN00021; CESP:F10F2.8
 pterinal source: clone F10F2
 metics:
 ne: CESP:F10F2.8
 IP position: 3
 trons: 46/3; 64/3; 151/1; 330/3; 365/2; 453/1
 Query Match 74.5%; Score 35; DB 2; Length 580;
 best Local Similarity 50.0%; Pred. No. 8.9;
 tches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 1 GPCXXXFIR 10
 395 GPCPAGFLQY 404

submitted to the EMBL Data Library, March 1997
 A; Reference number: Z20145
 A; Accession: T26063
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-2225 <WIL>
 A; Cross-references: EMBL:Z92815; PIDN:CAB07294.1; GSPDB:GN00023; CESP:W01F3.3
 A; Experimental source: clone W01F3
 C; Genetics:
 A; Gene: CESP:W01F3.3
 A; Map Position: 5
 A; Introns: 33/1; 56/1; 100/1; 142/3; 271/3; 451/1; 525/3; 774/1; 1093/1; 1178/1; 1221/1;
 Query Match 74.5%; Score 35; DB 2; Length 2225;
 best Local Similarity 60.0%; Pred. No. 29;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GPCXXXFIRY 10
 DB 470 GPCCHGSFQRY 479

RESULT 15
 J68704
 NHC c5/gll protein - mouse (fragment)
 C; Species: Mus musculus (house mouse)
 C; Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
 C; Accession: I68704
 R; Rogers, J.H.
 Immunogenetics 21, 343-353, 1985
 A; Title: Family organization of mouse H-2 class I genes.
 A; Reference number: 154413; MUID:85206117; PMID:3997208
 A; Accession: I68704
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-91 <RES>
 A; Cross-references: GB:M14828; NID:g199643; PIDN:AAA39688.1; PID:g554240
 C; Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 72.3%; Score 34; DB 2; Length 91;
 best Local Similarity 50.0%; Pred. No. 2.9;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GPCXXXFIRY 10
 DB 71 GPCKDSLRY 80

Search completed: August 11, 2004, 13:09:58
 Job time : 10.9524 secs

JLT 14
)63)theoretical protein W01F3.3 - *Caenorhabditis elegans*
)species: *Caenorhabditis elegans*
)date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
)session: T26063
)immings, P.



Query Match 89.4%; Score 42; DB 1; Length 122;
 Best Local Similarity 60.0%; Pred. No. 0.019;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPCXXXFIRY 10
 Db 45 GPCSAHFVRY 54

RESULT 2
 BTI14_BOOMI STANDARD PRT; 25 AA.
 ID_BT14_BOOMI STANDARD; PRT; 25 AA.
 AC_P83605; DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Boophilus microplus (Cattle tick).
 OS Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 Parasitiformes; Ixodida; Ixodidae; Boophilus.
 OC NCBITaxID=6941;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=Larva;
 RA Sasaki S.D., Hirata I.Y., Tanaka A.S.;
 RT "Molecular studies of serine protease inhibitors from cattle tick
 Boophilus microplus (larvae)".
 RL Submitted (JUN-2003) to Swiss-Prot.
 CC -!- FUNCTION: Inhibits trypsin, human plasma kallikrein and human
 neutrophil elastase.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR InterPro; IPR002223; Kunitz_BPTI.
 PROSITE; PS00280; BPTI_KUNITZ_1; PARTIAL.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; PARTIAL.
 KW Serine protease inhibitor.
 ACT SITE 18 19 REACTIVE BOND (BY SIMILARITY).
 FT NON-TER 25 25
 SEQUENCE 25 AA; 2963 MW; B1CB3A2D2E121F3D CRC64;

Query Match 78.7%; Score 37; DB 1; Length 25;
 Best Local Similarity 60.0%; Pred. No. 0.051;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GPCXXXFIRY 10
 Db 15 GPCVGYFFRY 24

RESULT 3
 IBPS_BOVIN STANDARD PRT; 60 AA.
 ID_IBPS_BOVIN STANDARD; PRT; 60 AA.
 AC_P00975; DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Serum basic protease inhibitor (Serum BPI).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Fecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 RN [1]
 RP

RX RA MEDLINE=81044408; PubMed=7428928;
RX RA Wachter E., Depner K., Hochstrasser K., Lempart K., Geiger R.;
RT RT "A new Kunitz-type inhibitor from bovine serum amino acid sequence
 determination."
RT RT FEBS Lett. 119:58-62 (1980).
CC -!- CC FUNCTION: This inhibitor has activity very similar to that of the
 basic protease inhibitor from bovine tissues.
CC -!- CC SUBCELLULAR LOCATION: Secreted.
CC -!- CC SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR DR PIR; A01206; TIBOR.
DR DR HSSP; P00974; 1BPI.
DR DR InterPro; IPR002223; Kunitz_BPTI.
DR DR Pfam; PF00014; Kunitz_BPTI; 1.
DR DR PRINTS; PR000759; BASICFTASE.
DR DR PRODOM; PD000222; Kunitz_BPTI; 1.
DR DR SMART; SM00131; KU; 1.
DR DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT FT DISULFID 7 57 BY SIMILARITY.
FT FT DISULFID 16 40 BY SIMILARITY.
FT FT DISULFID 32 53 BY SIMILARITY.
FT FT ACT SITE 17 18 REACTIVE BOND.
SQ SQ SEQUENCE 60 AA; 6647 MW; B9953EBACF1A4E6 CRC64;
Query Match 78.7%; Score 37; DB 1; Length 60;
Best Local Similarity 60.0%; Pred. No. 0.12;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GPCXXXFIRY 10
 Db 14 GPCKAAAMIRY 23

RESULT 4
 EPPI_MACMU STANDARD PRT; 133 AA.
 ID_EPPI_MACMU STANDARD; PRT; 133 AA.
 AC_Q9BDL1; DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Eppin precursor (Epidymal protease inhibitor) (Serine protease
 inhibitor-like with Kunitz and WAP domains 1).
 GN SPINLWL.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopithecinae; Macaca.
 OC NCBITaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Epidymis, and Testis;
 RA Sivasharmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
 RA Richardson R.T.;
 RT "Characterization of monkey and mouse Eppin, a protease inhibitor from
 epididymis and testis.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN EPIDIDYMIS AND TESTIS.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -!- SIMILARITY: Contains 1 WAP-type domain.

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 or send an email to license@isb-sib.ch).

DR DR EMBL; AF346414; AAK31336.1; -.
DR DR HSSP; P00974; 1BPI.
DR DR InterPro; IPR002223; Kunitz_BPTI.

InterPro; IPR008197; WAP.
 Pfam; PF00014; Kunitz_BPTI; 1.
 PRINTS; PR00095; wap; 1.
 PRODOM; PR00759; BASICPTASE.
 PROSITE; PS00222; Kunitz_BPTI; 1.
 Serine protease inhibitor; Signal.
 SMART; SM00131; KU; 1.
 SMART; SM00217; WAP; 1.
 PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 SIGNAL 1 21 POTENTIAL.
 CHAIN 22 133 EPPIN.
 DOMAIN 29 73 WAP.
 DOMAIN 77 127 BPTI/KUNITZ INHIBITOR.
 DISULFID 33 61 BY SIMILARITY.
 DISULFID 40 65 BY SIMILARITY.
 DISULFID 48 60 BY SIMILARITY.
 DISULFID 54 69 BY SIMILARITY.
 DISULFID 77 127 BY SIMILARITY.
 DISULFID 86 110 BY SIMILARITY.
 DISULFID 102 123 BY SIMILARITY.
 SEQUENCE 133 AA; 15279 MW; 433AE946E39A35E9 CRC64;

very Match 78.7%; Score 37; DB 1; Length 133;
 1st Local Similarity 60.0%; Pred. No. 0.27;
 Itches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

JLT 5
 BPT1_BOVIN STANDARD; PRT; 100 AA.
 P00974; 21-JUL-1986 (Rel. 01, Created)
 01-MAR-1989 (Rel. 10, Last sequence update)
 10-OCT-2003 (Rel. 42, Last annotation update)
 Pancreatic trypsin inhibitor precursor (Basic protease inhibitor)
 (BPI) (BPTI) (Aprotinin).
 Bos taurus (Bovine).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Peccora; Bovoidea;
 Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913; [11]

SEQUENCE FROM N.A.
 MEDLINE=87283904; PubMed=2441071;
 Creighton T.E., Charles I.G.; "Biosynthesis, processing, and evolution of bovine trypsin inhibitor." Sequences of the genes and polypeptide precursors for two bovine protease inhibitors." J. Mol. Biol. 194:11-22 (1987). [12]

SEQUENCE FROM N.A.
 MEDLINE=88295740; PubMed=2456884;
 Creighton T.E., Charles I.G.; "Biosynthesis, processing, and evolution of bovine pancreatic trypsin inhibitor." Sequences encoding two trypsin inhibitors occur in strikingly similar genomic environments." Biochem. J. 233:443-450 (1986). [13]

SEQUENCE OF 34-97 FROM N.A.
 MEDLINE=86158754; PubMed=2420326;
 Kingston I.B., Anderson S.; "Isolation of a genomic clone for bovine pancreatic trypsin inhibitor by using a unique-sequence synthetic DNA probe." Biochem. J. 233:443-450 (1986). [14]

Proc. Natl. Acad. Sci. U.S.A. 80:6838-6842 (1983). [5]
 RP SEQUENCE OF 36-93, AND DISULFIDE BONDS.
 RX MEDLINE=66083012; PubMed=5860161;
 RA Kassell B., Laskowski M.; "The basic' trypsin inhibitor of bovine pancreas. V. The disulfide linkages." Biochem. Biophys. Res. Commun. 20:463-468 (1965). [6]
 RP SEQUENCE OF 36-93, AND DISULFIDE BONDS.
 RX MEDLINE=66171231; PubMed=5296424;
 RA Anderer F.A., Hornig S.; "The disulfide linkages in kallikrein inactivator of bovine lung." J. Biol. Chem. 241:1568-1572 (1966). [7]
 RP SEQUENCE OF 36-93, AND DISULFIDE BONDS.
 RX MEDLINE=68012003; PubMed=6053284;
 RA Chauvet J., Achter R.; "Covalent structure of a polypeptide inhibitor of trypsin (Kunitz and Northrop inhibitor)." Bull. Soc. Chim. Biol. 49:985-1000 (1967). [8]
 RP SEQUENCE OF 36-93.
 RA Dlouha V., Pospisilova D., Meloun B., Sorm F.; "Sequence of residues 18-20 in pancreatic trypsin inhibitor." Collect. Czech. Chem. Commun. 33:1363-1365 (1968). [9]
 RP SEQUENCE OF 36-81.
 RC TISSUE=Adrenal chromaffin; [10]
 RX MEDLINE=90211226; PubMed=2322242;
 RA Lewis R.V., Ray P., Coguill R.; Kruggel W.; "Presence of pancreatic trypsin inhibitor in adrenal medullary chromaffin cells." Acta Crystallogr. B 31:238-250 (1975). [11]
 RL Bichem. Biophys. Res. Commun. 167:543-547 (1990). [12]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RA Deisenhofer J., Steigemann W.; "Crystallographic refinement of the structure of bovine pancreatic trypsin inhibitor at 1.5-A resolution." Acta Crystallogr. B 31:238-250 (1975). [13]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=70255230; PubMed=5447861;
 RA Huber R., Kukla D., Ruhmann A., Epp O., Formanek H.; "The basic trypsin inhibitor of bovine pancreas. I. Structure analysis and conformation of the polypeptide chain." Naturwissenschaften 57:389-392 (1970). [14]
 RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF MUTANT GLY-70.
 RX MEDLINE=91332906; PubMed=1714504;
 RA Houssset D., Kim K.-S., Fuchs J.; Woodward C., Wlodawer A.; "Crystal structure of a Y35G mutant of bovine pancreatic trypsin inhibitor." J. Mol. Biol. 220:757-770 (1991). [15]
 RN STRUCTURE BY NMR.
 RX MEDLINE=93021116; PubMed=1383552;
 RA Berndt K.D., Gunter P., Orbons L.P.M., Wuethrich K.; "Determination of a high-quality nuclear magnetic resonance solution structure of the bovine pancreatic trypsin inhibitor and comparison with three crystal structures." J. Mol. Biol. 227:757-775 (1992). [16]
 CC -!- FUNCTION: Inhibits trypsin, kallikrein, chymotrypsin, and plasmin.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PHARMACEUTICAL: Available under the name Trasylol (Mile). Used for inhibiting coagulation so as to reduce blood loss during bypass surgery.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -!- DATABASE: NAME=Trasylol; NORC=Clinical information on Trasylol; WWW="http://www.trasylol.com".
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CC	DR	PROSITE; PS50279; BPTI_KUNITZ_2; 1.
CC	KW	Serine protease inhibitor; Signal; Pharmaceutical; 3D-structure.
CC	FT	SIGNAL 1 21
CC	FT	PROPEP 22 35
CC	FT	CHAIN 36 93
CC	FT	PROPEP 94 100
CC	FT	BPTI/KUNITZ INHIBITOR.
DR	EMBL; M20934; AAD13685.1; -.	
DR	EMBL; M20930; AAD13685.1; JOINED.	
DR	EMBL; M20932; AAD13685.1; JOINED.	
DR	EMBL; X03365; CAA27062.1; ALT_SEQ.	
DR	EMBL; X03365; CAA27063.1; -.	
DR	EMBL; X05274; CAA2B886.1; -.	
PIR	PIR; S00277; TIBO.	
DR	PDB; 1TPA; 14-MAR-85.	
DR	PDB; 2PTC; 14-MAR-85.	
DR	PDB; 4PTI; 16-APR-87.	
DR	PDB; 5PTI; 15-JAN-90.	
DR	PDB; 6PTI; 16-JAN-88.	
DR	PDB; 7PTI; 15-APR-91.	
DR	PDB; 8PTI; 15-OCT-91.	
DR	PDB; 9PTI; 15-OCT-92.	
DR	PDB; 2TGPF; 14-MAR-85.	
DR	PDB; 2TP1; 15-JUL-91.	
DR	PDB; 3TP1; 14-MAR-85.	
DR	PDB; 4TP1; 08-NOV-85.	
DR	PDB; 1AAL; 31-OCT-93.	
DR	PDB; 1BPT; 15-JAN-93.	
DR	PDB; 1BT1; 31-OCT-93.	
DR	PDB; 1FAN; 31-OCT-93.	
DR	PDB; 1NAG; 31-OCT-93.	
DR	PDB; 2KAI; 15-OCT-91.	
DR	PDB; 1PIT; 31-JAN-94.	
DR	PDB; 1BRB; 31-JUL-94.	
DR	PDB; 1BPI; 03-JUN-95.	
DR	PDB; 1MTN; 17-AUG-96.	
DR	PDB; 1BTH; 24-DEC-97.	
DR	PDB; 1CBW; 23-JUL-97.	
DR	PDB; 1B0C; 11-NOV-98.	
DR	PDB; 1BZ5; 11-NOV-98.	
DR	PDB; 3TGI; 23-DEC-98.	
DR	PDB; 3TGJ; 23-DEC-98.	
DR	PDB; 1FAK; 03-DEC-99.	
DR	PDB; 1BHC; 16-SEP-98.	
DR	PDB; 1BZX; 29-DEC-99.	
DR	PDB; 1CO7; 07-JAN-03.	
DR	PDB; 1D0D; 09-SEP-00.	
DR	PDB; 1F5R; 04-JUL-01.	
DR	PDB; 1F7Z; 04-JUL-01.	
DR	PDB; 1FY8; 04-JUL-01.	
DR	PDB; 1JV8; 27-FEB-02.	
DR	PDB; 1JV9; 27-FEB-02.	
DR	PDB; 1K6U; 19-DEC-01.	
DR	PDB; 1LDS; 11-SEP-02.	
DR	PDB; 1LD6; 11-SEP-02.	
DR	PDB; 1QLQ; 03-FEB-00.	
DR	PDB; 2HEX; 11-MAR-03.	
DR	PDB; 3BTD; 13-MAR-00.	
DR	PDB; 3BTE; 15-MAR-00.	
DR	PDB; 3BTF; 13-MAR-00.	
DR	PDB; 3BTG; 13-MAR-00.	
DR	PDB; 3BTH; 13-MAR-00.	
DR	PDB; 3TGF; 04-JUL-01.	
DR	InterPro; IPR002223; Kunitz_BPTI.	
DR	PFam; PF00014; Kunitz_BPTI; 1.	
DR	PRINTS; PR00759; BASICPTASE.	
DR	ProDom; PD000222; Kunitz_BPTI; 1.	
DR	SMART; SM00131; KU; 1.	
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.	
DR	PROSITE; PS50279; BPTI_KUNITZ_2; 1.	
DR	SEQUENCE FROM N.A.	
DR	MEDLINE=87283904; PubMed=2441071;	
RA	Creighton T.E., Charles I.G.;	
RT	"Sequences of the genes and polypeptide precursors for two bovine spleen trypsin inhibitors I, II, and III precursor (SI)."	
RL	Bos taurus (Bovine).	
RN	OS	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Butheroidea; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;	
OC	Bovidae; Bovinae; Bos.	
NCBI_TaxID=9913;		
[1]	SEQUENCE FROM N.A.	
RN	MEDLINE=88295740; PubMed=245684;	
RX	Creighton T.E., Charles I.G.;	
RT	"Biosynthesis, processing, and evolution of bovine pancreatic trypsin inhibitor."	
RL	J. Mol. Biol. 194:11-22 (1987).	
RN	[2]	
RN	Cold Spring Harb. Symp. Quant. Biol. 52:511-519 (1987).	
RN	[3]	
RN	SEQUENCE OF 34-97 FROM N.A. (SI-I).	
RX	MEDLINE=86158754; PubMed=2420326;	
RA	Kingston I.B., Anderson S.;	
RT	"Sequences encoding two trypsin inhibitors occur in strikingly similar genomic environments."	
RL	Biochem. J. 233:443-450 (1986).	
RN	[4]	
RN	SEQUENCE OF 34-99 (SI-I).	
RX	MEDLINE=88007631; PubMed=2462435;	
RA	Fiorucci E., Angeletti M., Fiorucci L., Barra D., Bossa F., Ascoli F.;	
RT	"Primary structure of a protease isoInhibitor from bovine spleen. A possible intermediate in the processing of the primary gene product."	
RL	J. Biol. Chem. 262:13916-13919 (1987).	
RN	[5]	
RN	SEQUENCE OF 34-99 (SI-I).	
RX	MEDLINE=88007630; PubMed=3654647;	
RA	Barra D., Simmaco M., Angeletti M., Fiorucci E., Angeletti M., Ascoli F.;	
RT	"Primary structure of a protease isoInhibitor from bovine spleen. A possible intermediate in the processing of the primary gene product."	
RL	J. Biol. Chem. 262:13916-13919 (1987).	

[6] SEQUENCE OF 36-93 (SI-II).
MEDLINE=86008178; PubMed=2413011;
Fioretti E., Iacopino G., Angeletti M., Barra D., Bossa F., Ascoli F.;
"Primary structure and antiproteolytic activity of a Kunitz-type
inhibitor from bovine spleen."
J. Biol. Chem. 260:11451-11455(1985).

[7] SEQUENCE OF 36-97 (SI-III).
MEDLINE=91098258; PubMed=1986787;
Barra D., Fioretti E., Angeletti M., Maras B., Bossa F., Ascoli F.;
"Proteinase iso-inhibitors from bovine spleen: primary structure of an
intermediate in the processing of the precursor.";
Biochim. Biophys. Acta 1076:143-147(1991).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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EMBL; M20935; AAA51418_1; -.
EMBL; M20931; AAA51418_1; JOINED.
EMBL; M20933; AAA51418_1; JOINED.
EMBL; X05275; CAA28887_1; -.
EMBL; X06685; CAA29881_1; -.
EMBL; X03366; CAA27064_1; ALT_SEQ.
EMBL; X03366; CAA27065_1; -.
PIR; S00274; TIBOSP.
HSSP; P00974; 1BPI.
InterPro; IPR002223; Kunitz_BPTI.
PFam; PF00014; Kunitz_BPTI_1.
PRINTS; PRO0759; BASICPTASE.
PRODom; PD000222; Kunitz_BPTI_1.
SMART; SM00131; KU_1.
PROSITE; PS00280; BPTI_KUNITZ_1; 1.
PROSITE; PS50279; BPTI_KUNITZ_2; 1.
Serine protease inhibitor; Signal.
SIGNAL 1 21 POTENTIAL.
PROPEP 22 33 SPLEEN TRYPSIN INHIBITOR I.
CHAIN 34 99 SPLEEN TRYPSIN INHIBITOR II.
CHAIN 36 93 SPLEEN TRYPSIN INHIBITOR III.
DOMAIN 40 90 BPTI/KUNITZ INHIBITOR.
DISULFID 40 90 BY SIMILARITY.
DISULFID 49 73 BY SIMILARITY.
DISULFID 65 86 BY SIMILARITY.
ACT SITE 50 51 REACTIVE BOND (BY SIMILARITY).
SEQUENCE 100 AA; 10843 MW; 39069734BBACF4E3 CRC64;

every Match 76.6%; Score 36; DB 1; Length 100;
st Local Similarity 60.0%; Pred. No. 0.33; Indels 0; Gaps 0;

tches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 GPCXXXFIRY 10
• 47 GPCAKKMY 56

RESULT 8
ID_IBPI_TACTR STANDARD; PRT; 61 AA.
ID_IBPI_TACTR STANDARD; PRT; 61 AA.
AC P16044;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Proteinase inhibitor (BPI-type).
OS Tachypleus tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachypleus.
OX NCBI_TaxID=6853;
RN [1]
RP
RC TISSUE=Hemocyte;
RX MEDLINE=88007472; PubMed=3308864;
RA Nakamura T.; Hirai T.; Kawabata S.; Iwanaga S.;
RT "Purification and amino acid sequence of Kunitz-type protease
inhibitor found in the hemocytes of horseshoe crab (Tachypleus
tridentatus)." ;
RI J. Biochem. 101:1297-1306(1987).
CC -!- FUNCTION: Inhibitor of trypsin and chymotrypsin.
CC -!- SUBCELLULAR LOCATION: Secreted.

ILT 7

CSTI_BOMMO STANDARD; PRT; 55 AA.
P81902; 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Trypsin inhibitor (Cocoon shell-associated trypsin inhibitor) (CSTI).
Bombyx mori (Silk moth).
Eukaryotta; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
RN [1]
RP SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=Asahii;
RX MEDLINE=99115431; PubMed=9914483;
RA Kurioka A.; Yamazaki N.; Hirano H.;
RT "Primary structure and possible functions of a trypsin inhibitor of
Bombyx mori." ;
RT Eur. J. Biochem. 259:120-126(1999).
CC -!- FUNCTION: This cocoon shell-associated protein inhibits trypsin
Activity by forming a low-dissociation complex with trypsin. May
play an important part in regulating proteolytic activity in the
silk gland or protecting silk proteins from degradation during
histolysis.
CC -!- SUBUNIT: Monomer.
CC -!- TISSUE SPECIFICITY: Expressed exclusively in the middle silk
gland.
CC -!- DEVELOPMENTAL STAGE: Expression differentially regulated in the
middle silk glands during the final stage of larval growth with
highest expression before the onset of spinning.
CC -!- MASS SPECTROMETRY: MW=6658; METHOD=Electrospray.
CC -!- MISCELLANEOUS: Has an isoelectric point of 4.3.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC HSSP; P31713; 1SHP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI_1.
DR PRINTS; PRO0759; BASICPTASE.
DR PRODom; PD000222; Kunitz_BPTI_1.
DR SMART; SM00131; KU_1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Developmental protein; Serine protease inhibitor.
FT DISULFID 4 54 BY SIMILARITY.
FT DISULFID 13 37 BY SIMILARITY.
FT DISULFID 29 50 BY SIMILARITY.
FT ACT_SITE 14 15 REACTIVE BOND (TRYPSIN) (BY
SIMILARITY)
SQ SEQUENCE 55 AA; 6027 MW; C2739BBBF2BB6E59 CRC64;
Query Match 74.5%; Score 35; DB 1; Length 55;
Best Local Similarity 60.0%; Pred. No. 0.31;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 GPCXXXFIRY 10
Db 11 GPCCKGSFPRY 20

CC !- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; A26923; TIHCBP.
DR HSSP; P00974; 1BPI.
DR InterPro; IPR002223; Kunitz_BPTI.
DR PFam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR Serine protease inhibitor.
FT DISULFID .8 58 BY SIMILARITY.
FT DISULFID 17 41 BY SIMILARITY.
FT DISULFID 33 54 BY SIMILARITY.
FT ACT SITE 18 .19 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 61 AA; 6825 MW; 730E82CDD0653E4B CRC64;

Query Match 74.5%; Score 35; DB 1; Length 61;
Best Local Similarity 60.0%; Pred. No. 0.34;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GPCXXXFIRY 10
Db 15 GPCRAGFKRY 24

RESULT 9
IP52_ANESU STANDARD; PRT; 62 AA.
AC P10280; Rel. 10, Created
DT 01-MAR-1989 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 40, Last annotation update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protease inhibitor 5 II (SAS II).
OS Anemonia sulcata. (Snake-locks sea anemone)
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nymantheae; Actiniidae; Anemonia.
NCBI_TaxID=610B;
RN SEQUENCE OF 1-59.
RA Wunderer G., Machleidt W., Fritz H.;
RT "The broad-specificity proteinase inhibitor 5 II from the sea anemone
Anemonia sulcata.";
RT Meth. Enzymol. 80:816-820(1981).
RN [2]
RP SEQUENCE.
RA Krebs H.C., Habermehl G.G.;
RT "Isolation and structural determination of a hemolytic active peptide
from the sea anemone Metridium senile.";
RT Naturwissenschaften 74:395-396(1987).
CC !- FUNCTION: Inhibitor of Kallikreins.
CC !- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; S07451; S07451.
HSSP; P31713; 1SHP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR PFam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR Serine protease inhibitor.
FT DISULFID 5 55 BY SIMILARITY.
FT DISULFID 14 38 BY SIMILARITY.
FT DISULFID 30 51 BY SIMILARITY.
FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
FT VARIANT 13 13 P -> R.
FT VARIANT 16 16 A -> G.
FT VARIANT 17 17 R -> G.
FT VARIANT 25 25 S -> L.
FT VARIANT 28 28 K -> R.
FT VARIANT 39 39 G -> R.
SQ SEQUENCE 62 AA; 6937 MW; 7262D028CA567BC8 CRC64;

Query Match 74.5%; Score 35; DB 1; Length 62;
Best Local Similarity 60.0%; Pred. No. 0.35;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 GPCXXXFIRY 10
Db 12 GPCRARRFPY 21

RESULT 10
IBPC_BOVIN STANDARD; PRT; 67 AA.
ID IBPC_BOVIN
AC P00976; Rel. 01, Created
DT 21-JUL-1986 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 40, Last annotation update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DB Colostrum trypsin inhibitor (Colostrum BPI).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Peccora; Bovoidea;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
OX [1]

RN RP SEQUENCE.
RA Cechova D., Jonakova V., Sorm F.;
RT "Primary structure of trypsin inhibitor from cow colostrum (component
RT B2)";
RL Collect. Czech. Chem. Commun. 36:3342-3357 (1971).
RN RP DISULFIDE BONDS.
RA Cechova D., Ber E.;
RT "Disulfide bonds of trypsin inhibitor from cow colostrum.";
RL Collect. Czech. Chem. Commun. 39:680-688 (1974).
RN RP CHARACTERIZATION.
RA Cechova D., Muszynska G.;
RT "Role of lysine 18 in active center of cow colostrum trypsin
inhibitor.";
RT FEBS Lett. B:84-86 (1970).
RL PRODom; PD000222; Kunitz_BPTI.
CC !- SUBCELLULAR LOCATION: Secreted.
CC !- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; A01207; TIBOC.
DR HSSP; P02760; 1BIK.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor; Glycoprotein.
FT DISULFID 8 58
FT DISULFID 17 41
FT DISULFID 33 54
FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .).
FT ACT SITE 18 19 REACTIVE BOND (TRYPSIN).
SQ SEQUENCE 67 AA; 7511 MW; E2B2093B7CD207CD CRC64;

Query Match 74.5%; Score 35; DB 1; Length 67;
Best Local Similarity 50.0%; Pred. No. 0.38;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GPCXXXFIRY 10
Db 15 GPCKAALLRY 24

RESULT 11
MCPI_MELCP STANDARD; PRT; 197 AA.
ID MCPI_MELCP
AC P82968;
DT 28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)
 10-OCT-2003 (Rel. 42, Last annotation update)
 Melithaea calidonica.
 Eukaryota; Metazoa; Cnidaria; Anthozoa; Alcyonaria; Gorgonacea;
 Scleraxonia; Melithaeidae; Melithaea.
 NCBI_TAXID=156534;

[1] SEQUENCE, AND VARIANT VAL-195. Peduzzi J., Longeon A., Guyot M., Barthélémy M.; "Amino acid sequence and kinetic properties of a four-domain proteases inhibitor from the gorgonian Melithaea caledonica." Eur. J. Biochem. 0:0-0 (2001).

-!- FUNCTION: INHIBITS TRYPSIN, KALLIKREIN, SUBTILISIN CARLSBERG, HUMAN LEUKOCYTE ELASTASE, PORCINE PANCREATIC ELASTASE AND CHYMOTRYPSIN. TWO DOMAINS ARE FOR THE INHIBITION OF CHYMOTRYPSIN.

-!- SIMILARITY: Contains 3 Kazal-like domains.

-!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

HSSP; P31713; ISHP.

InterPro; IPR002350; kazal.

IPR002223; Kunitz_BPTI.

PFam; PF00050; kazal; 3.

SMART; SM00131; KU; 1.

PRINTS; PR00759; BASICPTASE.

ProDom; PD000222; Kunitz_BPTI; 1.

SMART; SM00280; KAZAL; 3.

SMART; SM00131; KU; 1.

PROSITE; PS00280; BPTI_KUNITZ_1; 1.

PROSITE; PS50279; BPTI_KUNITZ_2; 1.

PROSITE; PS00282; KAZAL; FALSE NEG.

Serine protease inhibitor; Repeat.

DOMAIN	1	45	KAZAL-LIKE 1.
DOMAIN	49	93	KAZAL-LIKE 2.
DOMAIN	97	141	KAZAL-LIKE 3.
DOMAIN	144	194	BPTI/KUNITZ INHIBITOR.
ACT_SITE	7	8	REACTIVE BOND 1 (BY SIMILARITY).
ACT_SITE	55	56	REACTIVE BOND 2 (BY SIMILARITY).
ACT_SITE	103	104	REACTIVE BOND 3 (BY SIMILARITY).
ACT_SITE	154	155	REACTIVE BOND 4 (BY SIMILARITY).
DISULFID	1	31	BY SIMILARITY.
DISULFID	5	24	BY SIMILARITY.
DISULFID	13	45	BY SIMILARITY.
DISULFID	49	79	BY SIMILARITY.
DISULFID	53	72	BY SIMILARITY.
DISULFID	61	93	BY SIMILARITY.
DISULFID	97	127	BY SIMILARITY.
DISULFID	101	120	BY SIMILARITY.
DISULFID	109	141	BY SIMILARITY.
DISULFID	144	194	BY SIMILARITY.
DISULFID	153	177	BY SIMILARITY.
DISULFID	169	190	BY SIMILARITY.
VARIANT	195	195	M -> V.

SEQUENCE 197 AA; 21248 MW; 199D08A489879579 CRC64;

every Match 74.5%; Score 35; DB 1; Length 197;
 st Local Similarity 60.0%; Pred. No. 1.1;
 tches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 GPCXXXFIR 10
 151 GPCRGAFFRY 160

LT 12
 SALTY STANDARD; PRT; 330 AA.

P26375; 01-AUG-1992 (Rel. 23, Created)
 01-AUG-1992 (Rel. 23, Last sequence update)
 28-FEB-2003 (Rel. 41, Last annotation update)
 RFBI protein.
 RFBI OR STM2093.
 Salmonella typhimurium.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX [1] _TAXID=602;
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=LT2;
 RX MEDLINE=91260454; PubMed=1710759;
 RA Jiang X.-M., Neal B., Santiago F., Lee S.J., Romana L.K., Reeves P.R.; "Structure and sequence of the rfb (O antigen) gene cluster of Salmonella serovar typhimurium (strain LT2)."
 RT Mol. Microbiol. 5:695-713 (1991).
 RL [2]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of *Salmonella enterica* serovar Typhimurium LT2." RL Nature 413:852-856 (2001).
 CC -!- PATHWAY: Lipopolysaccharide O antigen biosynthesis.
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 CC --- EMBL; AE008792; AAL20997.1; -. DR EMBL; AE008792; AAL20997.1; -. DR PIR; S15303; S15303.
 CC --- HSSP; P00235; 1FRR.
 CC --- StyGene; SG10451; rfbI.
 CC --- InterPro; IPR006058; 2FE2S fd BS. DR InterPro; IPR008333; FAD binding_6.
 CC --- InterPro; IPR001041; Ferredoxin. DR InterPro; IPR001709; FPN cyt reductase. DR InterPro; IPR001433; Oxred_FAD/NAD(P). DR InterPro; IPR001221; Phe hydroxylase. DR InterPro; IPR00970; FAD binding_6; 1. DR Pfam; PF00111; Fer2; 1. DR Pfam; PF00175; NAD binding_1; 1. DR PRINTS; PR00371; FPNCR.
 CC --- DR PRINTS; PR00410; PHEHYDROLKLASE.
 CC --- DR PROSITE; PS00197; 2FE2S_FERREDOXIN; UNKNOWN_1.
 CC --- KW Lipopolysaccharide biosynthesis; Complete proteome. SQ SEQUENCE 330 AA; 36582 MW; EFC1BBC17A0CCB2D CRC64;
 Query Match 74.5%; Score 35; DB 1; Length 330;
 Best Local Similarity 66.7%; Pred. No. 1.8;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GPCXXXFIR 9
 DB 184 GPCGTFFFIR 192

RESULT 13
 LT 13
 IATR_SHEEP STANDARD; PRT; 123 AA.
 AC P1371;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Inter-alpha-trypsin inhibitor (ITI) (GIK-14) (Inhibitory fragment of ITI) (Fragment).
 OS Ovis aries (Sheep) and
 OS Capra hircus (Goat).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 Bovidae; Caprinae; Ovis.
 NCBI_TaxID=9940, 9925;

[1] SEQUENCE.
 RP SPECIES=Sheep;
 RX MEDLINE=87299012; PubMed=2441725;
 RA Rasp G., Hochstrasser K., Wachter E., Reisinger P.W.M.;
 RT "The amino-acid sequence of the trypsin-released inhibitor from sheep
 inter-alpha-trypsin inhibitor."
 RL Biol. Chem. Hoppe-Seyler 368:727-731(1987).
 RN [2] SEQUENCE.
 RP SPECIES=C. hircus; PubMed=9010540;
 RX MEDLINE=9010540; PubMed=2481505;
 RA Rasp G., Hochstrasser K., Gerl C., Wachter E.;
 RT "Primary structure of a proteinase inhibitor released from goat serum
 inter-alpha-trypsin inhibitor."
 RL Biochim. Biophys. Acta 999:335-337(1989).
 CC -!- FUNCTION: This inhibitory fragment, released from native ITI after
 limited proteolysis with trypsin, contains two homologous domains.
 CC Whereas the second domain is a strong inhibitor of trypsin, the
 first domain interacts weakly with PMN-granulocytic elastase and
 CC not at all with pancreatic elastase.
 CC !- MISCELLANEOUS: The amino acid at position p2' (17) appears to
 CC determine the specificity of the inhibition of domain I.
 CC Inhibitors with methionine in this position interact weakly with
 CC chymotrypsin and elastase; those with leucine interact strongly.
 CC !- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
 DR PIR; A29652; A29652.
 DR HSSP; P02760; 1B1K.
 DR PRINTS; PR00759; BASICPTASE.
 DR PRODOM; PD000222; Kunitz_BPTI; 2.
 DR SMART; SM00131; KU; 2.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 2.
 KW Plasma; Glycoprotein; Serine protease inhibitor; Repeat.

FT NON_TER	1	1	BPTI/KUNITZ INHIBITOR 1.
FT DOMAIN	5	55	BPTI/KUNITZ INHIBITOR 1.
FT DOMAIN	61	111	BPTI/KUNITZ INHIBITOR-2.
FT DISULFID	5	55	BY SIMILARITY.
FT DISULFID	14	38	BY SIMILARITY.
FT DISULFID	30	51	BY SIMILARITY.
FT DISULFID	61	111	BY SIMILARITY.
FT DISULFID	70	94	BY SIMILARITY.
FT DISULFID	86	107	BY SIMILARITY.
FT SITE	15	16	INHIBITORY (P1) (CHYMOTRYPSIN, ELASTASE).
FT SITE	71	72	INHIBITORY (P1) (TRYPSIN).
FT CARBOHYD	24	24	N-LINKED (GLCNAC. .).
FT NON_TER	123	123	
SQ SEQUENCE	123 AA;	13686 MW;	295038173F22D2D1 CRC64;

Query Match 72.3%; Score 34; DB 1; Length 123;
 Best Local Similarity 60.0%; Pred. No. 1.1; Mismatches 4; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Gapopen 0; Gapclose 0;

[6] PARTIAL SEQUENCE OF 23-35; 47-53 AND 133-146.
 RP TISSUE=Placenta;
 RC MEDLINE=88106628; PubMed=3276312;
 RA Buetzow R., Huhtala M.-L., Bohn H., Virtanen I., Seppaela M.;
 RT "Purification and characterization of placental protein 5.";
 RL Biochem. Biophys. Res. Commun. 150:483-490(1988).

[7] RN ERRATUM.
 RP Buetzow R., Huhtala M.-L., Bohn H., Virtanen I., Seppaela M.;
 RA Biochem. Biophys. Res. Commun. 151:630-631(1988).

[8] CC -!- FUNCTION: Seems to inhibit trypsin, Factor VIIa/tissue factor,
 CC weakly factor Xa. Has no effect on thrombin.

[9] CC -!- SUBCELLULAR LOCATION: Secreted.

[10] CC -!- TISSUE SPECIFICITY: Umbilical vein endothelial cells, liver,

RESULT 14
 TFP2_HUMAN STANDARD; PRT; 235 AA.
 ID TFP2_HUMAN
 AC P48307;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Tissue factor pathway inhibitor 2 precursor (TFPI-2) (Placental
 protein 5) (PP5).

placenta, heart, pancreas, and maternal serum at advanced pregnancy.

-!- DOMAIN: This inhibitor contains three inhibitory domains.

-!- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.

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EMBL; D29992; BAA06272; 1; -. GO; GO:0005578; C:extracellular matrix; TAS. PROSITE; PS00280; BPTI_KUNITZ_1; 2. PROSITE; PS50279; BPTI_KUNITZ_2; 3. Serine protease inhibitor; Glycoprotein; Repeat; Signal; Blood coagulation; Polymorphism.

SIGNAL 1 22 TISSUE FACTOR PATHWAY INHIBITOR 2. CHAIN 23 235 BPTI/KUNITZ INHIBITOR 1. DOMAIN 36 86 BPTI/KUNITZ INHIBITOR 2. DOMAIN 96 149 BPTI/KUNITZ INHIBITOR 3. DOMAIN 158 208 POLY-LYS. DOMAIN 213 217 REACTIVE BOND (BY SIMILARITY). ACT_SITE 46 47 REACTIVE BOND (BY SIMILARITY). ACT_SITE 107 108 REACTIVE BOND (BY SIMILARITY). ACT_SITE 168 169 REACTIVE BOND (BY SIMILARITY).

DISULFID 36 86 BY SIMILARITY. DISULFID 45 69 BY SIMILARITY. DISULFID 61 82 BY SIMILARITY. DISULFID 96 149 BY SIMILARITY. DISULFID 106 130 BY SIMILARITY. DISULFID 122 145 BY SIMILARITY. DISULFID 158 208 BY SIMILARITY. DISULFID 167 191 BY SIMILARITY. DISULFID 183 204 BY SIMILARITY. CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL). CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL). VARIANT 102 102 V->A (in dbSNP:1804202). CONFLICT 23 23 D->A (IN REF. 6).

SEQUENCE 235 AA; 26934 MW; 975ABASC53P7C65F CRC64; ery Match 72.3%; Score 34; DB 1; Length 235; st Local Similarity 50.0%; pred. No. 2.2; tches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 GPCXXXFIRY 10 ||| :||| 43 GPCRALLRY 52

LT 15 BOVIN STANDARD; PRT; 352 AA.

DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE AMBP protein precursor [Contains: Alpha-1-microglobulin; Inter-alpha- trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30) (BI-14)]
 DE (Cumulus extracellular matrix stabilizing factor) (ESF).
 GN AMBP OR ITIL.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1] RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96201710; PubMed=8611630;
 RA Lindqvist A.; Aakerstrom B.;
 RT "Bovine alpha 1-microglobulin/bikunin. Isolation and characterization of liver cDNA and urinary alpha 1-microglobulin.";
 RL Biochim. Biophys. Acta 1306:98-106(1996).
 RN [2] RN
 RP SEQUENCE OF 227-349.
 RX MEDLINE=852255967; PubMed=2408637;
 RA Hochstrasser K.; Wachter E.; Albrecht G.J.; Reisinger P.;
 RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-trypsin inhibitor, X. The amino-acid sequences of the trypsin-released inhibitors from horse and pig inter-alpha-trypsin inhibitors.";
 RT Biol. Chem. Hoppe-Seyler 366:473-478(1985).
 RN [3] RN
 RP SEQUENCE OF 227-348.
 RX MEDLINE=84133807; PubMed=6199275;
 RA Hochstrasser K.; Wachter E.;
 RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-trypsin inhibitor, VII. Determination of the amino-acid sequence of the trypsin-released inhibitor from bovine inter-alpha-trypsin inhibitor.";
 RT Hoppe-Seyler's Z. Physiol. Chem. 364:1679-1687(1983).
 RN [4] RN
 RP SEQUENCE OF 206-219.
 RC TISSUE=Fetal serum;
 RX MEDLINE=92291130; PubMed=1376324;
 RA Chen L.; Mao S.-J.T.; Larsen W.J.;
 RT "Identification of a factor in fetal bovine serum that stabilizes the cumulus extracellular matrix. A role for a member of the inter-alpha-trypsin inhibitor family.";
 RT J. Biol. Chem. 267:12380-12386(1992).
 RN [5] RN
 RP REACTIVE SITES.
 RX MEDLINE=84133808; PubMed=6199276;
 RA Hochstrasser K.; Albrecht G.J.; Schoenberger O.L.; Wachter E.;
 RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-trypsin inhibitor, VII. Characterization of the bovine inhibitor as double-headed trypsin-elastase inhibitor.";
 RT Hoppe-Seyler's Z. Physiol. Chem. 364:1689-1696(1983).
 RT FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA AND ALBUMIN.
 CC -!- FUNCTION: Inter-alpha-trypsin inhibitor, present in plasma and urine, inhibits trypsin, plasmin, and lysosomal granulocytic elastase.
 CC -!- FUNCTION: MAY DIFFUSE INTO FOLLICULAR FLUID AFTER AN OVULATORY EXPANSION, THROUGH STABILIZATION OF THE CUMULUS EXTRACELLULAR MATRIX THUS SUPPORTING THE PROCESS OF OVULATION.
 CC -!- SUBUNIT: I-alpha-1 plasma protease inhibitors are assembled from one or two heavy chains (H1, H2 or H3) and one light chain, bikunin. Inter-alpha-inhibitor (I-alpha-I) is composed of H1, H2 and bikunin, inter-alpha-like inhibitor (I-alpha-LI) of H2 and bikunin, and pre-alpha-inhibitor (P-alpha-I) of H3 and bikunin (BY similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.

-!- PTM: The precursor is proteolytically processed into two separately functioning proteins.

-!- PTM: Alpha-1-microglobulin contains covalently linked brown-yellow chromophores (By similarity).

-!- SIMILARITY: In the N-terminal section; belongs to the lipocalin family.

-!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.

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CC U35642; AAB07599.1; - .
CC EMBL; U35642; AAB07599.1; - .
CC DR

Search completed: August 11, 2004, 13:08:06
Job time : 8.61905 secs

-!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC
-!- PTM: The precursor is proteolytically processed into two
CC
separately functioning proteins.
CC
-!- PTM: Alpha-1-microglobulin contains covalently linked brown-
CC
yellow chromophores (By similarity).
CC
-!- SIMILARITY: In the N-terminal section; belongs to the lipocalin
CC
family.
CC
-!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
CC

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or send an email to license@isb-sib.ch).

EMBL; U35642; AAB07599.1; -.
 PIR; S68149; TIBOBI.
 HSSP; P02760; IBIK.
 InterPro; IPR002223; Kunitz_BPTI.
 InterPro; IPR002345; Lipocalin.
 InterPro; IPR000566; Lipocalin_cytFABP.
 Pfam; PF00014; Kunitz_BPTI; 2.
 Pfam; PF00061; lipocalin; 1.
 PRINTS; PR00759; BASICPTASE.
 PRINTS; PR00179; LIPOCALIN.
 PRODOM; PD000222; Kunitz_BPTI; 2.
 SMART; SM00131; KU; 2.
 PROSITE; PS00280; BPTI_KUNITZ_1; 2.
 PROSITE; PS50279; BPTI_KUNITZ_2; 2.
 PROSITE; PS00213; LIPOCALIN; 1.
 Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
 Lipocalin

LIPOCARIN.		19
SIGNAL	203	203
CHAIN	352	352
CHAIN	206	206
DOMAIN	231	281
DOMAIN	287	337
BINDING	53	53
BINDING	111	111
BINDING	137	137
BINDING	149	149
DISULFID	91	188
DISULFID	231	281
DISULFID	240	264
DISULFID	256	277
DISULFID	287	337
DISULFID	296	320
DISULFID	312	333
SITE	241	242
SITE	297	298
CARBOHYD	115	115
CARBOHYD	223	223
CARBOHYD	250	250
CONFLICT	209	209
CONFLICT	217	217
CONFLICT	268	268
CONFLICT	274	274
CONFLICT	298	299
CONFLICT	330	330
CONFLICT	346	346
SEQUENCE	352	352
BY SIMILARITY.		
ALPHA-1 MICROGLOBULIN.		
INTER-ALPHA-TRYPSIN INHIBITOR LIGHT CHAIN.		
BPTI/KUNITZ INHIBITOR 1.		
BPTI/KUNITZ INHIBITOR 2.		
CHROMOPHORE (BY SIMILARITY).		
BY SIMILARITY.		
INHIBITORY (P1) (CHYMOTRYPSIN, ELASTIN).		
INHIBITORY (P1) (TRYPSIN).		
N-LINKED {GLCNAC. .} (POTENTIAL).		
N-LINKED {GLCNAC. .} (POTENTIAL).		
N-LINKED {GLCNAC. .} (POTENTIAL).		
T -> G (IN REF. 4).		
A -> D (IN REF. 4).		
G -> L (IN REF. 2 AND 3).		
E -> Q (IN REF. 2 AND 3).		
SY -> AF (IN REF. 2 AND 3).		
E -> Q (IN REF. 2 AND 3).		
E -> R (IN REF. 2 AND 3).		
E0321CE5CA02B20819 CPC64.		

Query Match Best Local Similarity Score 34; Pred. No. 3.2; Length 352;

QY 1 GPCXXXFIRY 10
Dp 238 GPCCLSTEFIRY 242

rotein - protein search, using sw model

on: August 11, 2004, 13:04:18 ; Search time 31.9048 Seconds
 (without alignments)
 98.894 Million cell updates/sec

e: US-10-661-207-1
 ect score: 47
 tence: 1 GPCXXXFIRY 10

ing table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

ched: 1017041 seqs, 315518202 residues

1 number of hits satisfying chosen parameters: 1017041

num DB seq length: 0
 num DB seq length: 2000000000

-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

base : SPTREMBL_25:
 1: sp_archea:
 2: sp_bacteria:
 3: sp_fungi:
 4: sp_human:
 5: sp_invertebrate:
 6: sp_mammal:
 7: sp_mhc:
 8: sp_organelle:
 9: sp_phage:
 10: sp_plant:
 11: sp_rabbit:
 12: sp_virus:
 13: sp_vertebrate:
 14: sp_unclassified:
 15: sp_rvirus:
 16: sp_bacteriaph:
 17: sp_archeap:

17 34 72.3 273 7 Q860A2 mus abbotti
 18 34 72.3 273 7 Q860AO mus abbotti
 19 34 72.3 273 7 Q852Z8 mus cookii
 20 34 72.3 273 7 Q852Z7 mus cookii
 21 34 72.3 273 7 Q852Z5 mus dunni (Q852Z4 mus musculu
 22 34 72.3 273 7 Q852Z4 mus musculu
 23 34 72.3 273 7 Q852Z2 mus musculu
 24 34 72.3 273 7 Q852Z0 mus musculu
 25 34 72.3 273 7 Q852Y9 mus musculu
 26 34 72.3 273 7 Q852Y8 mus musculu
 27 34 72.3 273 7 Q852Y7 mus pahari
 28 34 72.3 273 7 Q852Y6 mus platyth
 29 34 72.3 273 7 Q852Y5 mus platyth
 30 34 72.3 273 7 Q852Y4 mus platyth
 31 34 72.3 273 7 Q852Y2 mus setulos
 32 34 72.3 273 7 Q852Y1 mus setulos
 33 34 72.3 273 7 Q852Y0 mus shortri
 34 34 72.3 273 7 Q852X9 mus shortri
 35 34 72.3 352 11 Q70160 cavia porce
 36 34 72.3 384 7 Q95551 mus musculu
 37 34 72.3 384 7 Q31202 mus musculu
 38 34 72.3 384 7 Q8HwB4 mus musculu
 39 34 72.3 384 11 Q60678 mus musculu
 40 34 72.3 395 11 Q8CGD8
 41 34 72.3 410 10 Q9C6V1
 42 34 72.3 431 10 Q8RWY1
 43 33 70.2 82 5 Q8MVb4
 44 33 70.2 407 16 Q8a456
 45 33 70.2 605 5 Q965Q9

ALIGNMENTS

RESULT 1
 Q8HZ45 ID Q8HZ45
 AC DT 01-MAR-2003 (TREMBrel. 23, Created)
 DT 01-MAR-2003 (TREMBrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
 DE Epididymal protease inhibitor 1.
 GN EPPIN.
 OS Papio papio (Guinea baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopithecinae; Papio.
 NCBI_TaxID=100937;
 [1] RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Testis;
 RC O'Rand M.G., Richardson R.T.;
 RA Sivashanmugam P., O'Rand M.G., Richardson R.T.;
 RT "Characterization Of Mouse Eppin And A Gene Cluster Of Similar
 Protease Inhibitors On Mouse Chromosome 2 Gene.";
 RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
 EMBL; AY141973; AA0N08507.1; -.
 DR GO; GO:0008233; F:peptidase inhibitor activity; IEA.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR InterPro; IPR008197; WAP.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1;
 DR PROSITE; PS50279; BPTI_KUNITZ_2;
 DR Protease.
 SQ SEQUENCE 133 AA; 15277 MW; B33AEE57ECBEBE84 CRC64;

SUMMARIES

lo.	Score	Query	Match	Length	DB	ID	Description
1	37	78.7	133	6	Q8HZ45		Q8hz45 Papio papio Q96888 Galleria me
2	36	76.6	76	5	Q96858		Q95s22 drosophila
3	36	76.6	461	5	Q95s22		Q9xz0 drosophila
4	36	76.6	763	5	Q9XZD0		Q8t719 bombyx mori
5	35	74.5	76	5	Q8T7L9		Q8z5i3 salmonella
6	35	74.5	324	16	Q8Z5I3		Q19315 caenorhabdi
7	35	74.5	580	5	Q19315		O458B1 caenorhabdi
8	35	74.5	2225	5	Q458B1		O19474 mus musculu
9	34	72.3	91	7	Q19474		Q8nak6 homo sapien
10	34	72.3	224	4	Q8NAK6		Q62323 mus musculu
11	34	72.3	253	11	Q62323		Q860a4 mus caroli
12	34	72.3	272	7	Q860A4		Q860a1 mus abbotti
13	34	72.3	272	7	Q860A1		Q85zz9 mus caroli
14	34	72.3	272	7	Q85ZZ9		Q85zz6 mus dunni (Q8hw12 rattus norv
15	34	72.3	272	7	Q85ZZ6		
16	34	72.3	273	7	Q8HW12		

Query Match Score 78.7%; DB 6; Length 133;
 Best Local Similarity 60.0%; Pred. No. 0.79%;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY	1	GPCXXXFIRY 10 84 GPCLAFFIRW 93	PRT;	76 AA.
DB	RESULT 2	Q968SB ID Q968SB AC Q968SB; DT 01-DEC-2001 (TREMBLrel. 19, Created) DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update) DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update) RA Silk protease inhibitor 1 precursor. DE Galleria mellonella (Wax moth). OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea; Pyralidae; Galleriinae; Galleria. NCBI_TaxID=7137;	[1]	SEQUENCE FROM N.A. MEDLINE=21175824; PubMed=11277929; RX Nirmala X.; Kodrik D.; Zurovec M.; Sehnal F.; RA "Insect silk contains both a Kunitz-type and a unique Kazal-type proteinase inhibitor."; RT Eur. J. Biochem. 268:2064-2073 (2001). RL EMBL; AF292098; AAK40037.1; DR GO; GO:0008233; F:Peptidase activity; IEA. DR GO; GO:0004867; F:Serine protease inhibitor activity; IEA. DR InterPro; IPR002223; Kunitz_BPTI. PFam; PF00014; Kunitz_BPTI_1. PRINTS; PRO00759; BASICPTASE. DR ProDom; PDO002222; Kunitz_BPTI_1. DR SMART; SM00131; KU; 1. DR PROSITE; PS00280; BPTI_KUNITZ_1; 1. DR PROSITE; PS50279; BPTI_KUNITZ_2; 1. DR protease; Protease inhibitor; Serine protease inhibitor; Signal. KW protease; Protease inhibitor; Serine protease inhibitor; Signal. FT SIGNAL 1 20 POTENTIAL. SQ SEQUENCE 76 AA; 8419 MW; OC6ED52550632B79 CRC64; RT "The genome sequence of <i>Drosophila melanogaster</i> ." RL Science 287:2185-2195 (2000).
RC	RC	PRELIMINARY;	76 AA.	RN [3]
RX	RX	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.	RN [4]
RA	RA	RP MEDLINE=20196006; PubMed=10731132;	RP SEQUENCE FROM N.A.	RN [5]
RA	RA	RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N., George R.A., Lewis S.E., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Blazej R.G., Champe M., Pfeiffer B.D., Brandon R.C., Rogers Y.-H.C., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abrial J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra T., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Gloeck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier B., Spradling A.C., Stapleton M., Strong R., Sun E., Wang X., Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; RT "The genome sequence of <i>Drosophila melanogaster</i> ." RL Science 287:2185-2195 (2000).	RP SEQUENCE FROM N.A.	RN [6]
RA	RA	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.	RN [7]
RA	RA	RA Adams M.D., Kronmiller B., Wan K.H., Holt R.A., Celniker S.E., Brandon R.C., Rogers Y., Evans C.A., Gocayne J.D., Amanatides P.G., Banzon J., Beeson K.Y., Busam D.A., Baldwin D., Banzon J., An H., Baldwin D., Beeson K.Y., Busam D.A., Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nuno J., Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M., "Sequencing of <i>Drosophila melanogaster</i> genome." RT Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.	RP SEQUENCE FROM N.A.	RN [8]
RA	RA	RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; "Annotation of <i>Drosophila melanogaster</i> genome." RT Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.	RP SEQUENCE FROM N.A.	RN [9]
RA	RA	RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.	RP SEQUENCE FROM N.A.	RN [10]
RA	RA	RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.	RP SEQUENCE FROM N.A.	RN [11]

[6] SEQUENCE FROM N.A.

FLYBase; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY060990; AAL28538.1; -.
EMBL; AE003804; AAM68494.1; -.
FLYBase; FBgn0026721; fat-spondin.
GO; GO:0004867; F:serine protease inhibitor activity; IEA.
InterPro; IPR000884; TSP1.
InterPro; IPR002223; Kunitz_BPTI.
PFam; PF00014; Kunitz_BPTI; 1.
PRINTS; PRO0759; BASICPTASE.
PRODom; PD000222; Kunitz_BPTI; 1.
BROSITE; PS00280; BPTI_KUNITZ_1; 1.
PROSITE; PS50279; BPTI_KUNITZ_2; 1.
PROSITE; PS50092; TSP1; 4.
Protein inhibitor; Serine protease inhibitor; IEA.
SEQUENCE 461 AA; 51517 MW; B77D07F41DD681B1 CRC64;

Very Match 76.6%; Score 36; DB 5; Length 461;
1st Local Similarity 50.0%; Pred. No. 4.3;
Itches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 GPCXXXFIRY 10
||| :|||
349 GPCRGTMYRY 358

1D0 PRELIMINARY; PRT; 763 AA.

Q9XZD0 PRELIMINARY; PRT; 763 AA.
01-NOV-1999 (TREMBLrel. 12; Created)
01-NOV-1999 (TREMBLrel. 12; Last sequence update)
01-JUN-2003 (TREMBLrel. 24; Last annotation update)

Fat-spondin protein.

FAT-SPONDIN OR CG6953.

Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydriodea; Drosophilidae; Drosophila.
NCBI_TaxID=7227; [1]

SEQUENCE FROM N.A.

STRAIN=Berkeley; MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Harris M.,
de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunn P.,
Durbin R.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Giodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Houck J.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Howick J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milashina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

[2]
RN SEQUENCE FROM N.A.
RC STRAIN=OREGON-R;
RA Darocha S.; Baumgärtner S.;
RT "Fat-Spondin, a Drosophila member of the Spondin family, is highly
expressed in fat body and hemocytes.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AE003804; AF057910.1; -.
HSSP; P00974; AF135119; ADD31715.1; -.
DR FLYBase; FBgn0026721; fat-spondin.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR000222; Kunitz_BPTI; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF02014; Reeler; 1.
DR Pfam; PF00090; tsp 1; 4.
DR PRINTS; PRO0759; BASICPTASE.
DR PRODom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KUJ; 1.
DR SMART; SM00209; TSP1; 4.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS50092; TSP1; 4.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 763 AA; 84945 MW; 3292DEDD2CFE4DAB CRC64;
Query Match 76.6%; Score 36; DB 5; Length 763;
Best Local Similarity 50.0%; Pred. No. 7;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GPCXXXFIRY 10
Db 651 GPCRGTMYRY 660

RESULT 5
Q8T7L9 PRELIMINARY; PRT; 76 AA.
ID Q8T7L9; AC Q8T7L9;
DT 01-JUN-2002 (TREMBLrel. 21; Created)
DT 01-JUN-2002 (TREMBLrel. 21; Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24; Last annotation update)
DE Kazal-type serine proteinase inhibitor 1.
SP11.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21873253; PubMed=11881808;
RA Nirnala X., Mita K., Vanisree V., Zurovec M., Sehnal F.;
RT "Identification of four small molecular mass proteins in the silk of
Bombyx mori.";
RT Insect Mol. Biol. 10:437-445 (2001).
RL DR EMBL; AF352583; AAL83944.1; -.
GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR002223; Kunitz_BPTI.

DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR PRODom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 DR Protease inhibitor; Serine protease inhibitor.
 SEQUENCE 76 AA; 8445 MW; AA3F97D373535A3B CRC64;

Query Match 74.5%; Score 35; DB 5; Length 76;
 Best Local Similarity 60.0%; Pred. No. 1.4;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

RESULT 6
 Q8Z5I3 PRELIMINARY; PRT; 324 AA.
 ID Q8Z5I3; AC Q8Z5I3; DR 01-MAR-2002 (TREMBLrel. 20, Created)
 DR 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DR 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Putative reductase RfbI.
 GN RFB1 OR STY2303 OR T0779.
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Salmonella.
 OX NCBI_TAXID=601;
 RN [1] RP SEQUENCE FROM N.A.
 RC STRAIN=CT18; MEDLINE=21534947; PubMed=11677608;
 RX Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 RN [2] RP SEQUENCE FROM N.A.
 RC STRAIN=TY2 / ATCC 700931; MEDLINE=22531367; PubMed=12644504;
 RX Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
 RA Burland V., Kodoyiani V., Schwartz D.C., Blattner F.R.;
 RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
 and CT18."
 RL J. Bacteriol. 185:2330-2337 (2003).
 DR EMBL; AL627273; CAD02456.1; -.
 DR EMBL; AE016036; AAO68470.1; -.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR InterPro; IPR006118; P:electron transport; IEA.
 DR InterPro; IPR006058; 2Fe2S Fd BS.
 DR InterPro; IPR008333; FAD-binding_6.
 DR InterPro; IPR001041; Ferredoxin.
 DR InterPro; IPR001709; FPN_cyt_redctse.
 DR InterPro; PF001433; Oxred_FAD/NAD(P).
 DR InterPro; IPR001221; Phe_hydroxylase.
 DR Pfam; PF00970; FAD_binding_6; 1.
 DR Pfam; PF00111; Fer2; 1.
 DR Pfam; PF00175; NAD_binding_1; 1.
 DR PRINTS; PRO0371; FPNCR.
 DR PRINTS; PRO0410; PHEHYDRXLASE.
 DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
 DR Hypothetical protein; Complete proteome.
 KW

SQ SEQUENCE 324 AA; 35884 MW; E3A556150FSCE199 CRC64;
 Query Match 74.5%; Score 35; DB 16; Length 324;
 Best Local Similarity 66.7%; Pred. No. 5.4;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPCXXXFIR 9
 Db 184 GPCGTFIFIR 192

RESULT 7
 Q19315 PRELIMINARY; PRT; 580 AA.
 ID Q19315; AC Q19315; DR 01-NOV-1996 (TREMBLrel. 01, Created)
 DR 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE F10F2.8 protein.
 GN F10F2.8.

OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelerinae; Caenorhabditis.
 OX NCBI_TAXID=6239;
 RN [1] RP SEQUENCE FROM N.A.
 RA Coles L.; DR Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
 RN [2] RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode *C.elegans*: A platform for
 investigating biology";
 RL Science 282:2012-2018(1998).
 DR EMBL; Z35598; CAA84654.1; -.
 DR PIR; T20716; T20716.
 DR WormPep; F10F2.B; CB00953.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
 SQ SEQUENCE 580 AA; 08687AC6C55A7FDF CRC64;

Query Match 74.5%; Score 35; DB 5; Length 580;
 Best Local Similarity 50.0%; Pred. No. 9.2;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPCXXXFIR 10
 Db 395 GPCPAGFLQY 404

RESULT 8
 Q45881 PRELIMINARY; PRT; 2225 AA.
 ID Q45881; AC Q45881; DR 01-JUN-1998 (TREMBLrel. 06, Created)
 DR 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE W01F3.3 protein.
 GN W01F3.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelerinae; Caenorhabditis.
 OX NCBI_TAXID=6239;
 RN [1] RP SEQUENCE FROM N.A.
 RA Cummings P.N.; DR Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
 RN [2] RP SEQUENCE FROM N.A.

MEDLINE=99069613; PubMed=9851916;
none;
"Genome sequence of the nematode *C.elegans*: A platform for investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z92815; CAB07294.1; -.
PIR; T26063; T26063.
HSSP; P31713; 1SHP.
WormPep; W01F3.3; CE16531.
GO; GO:0004867; F:serine protease inhibitor activity; IEA.
InterPro; IPR002223; Kunitz_BPTI.
InterPro; IPR000716; Thryroglobulin_1.
InterPro; IPR006150; Worm repeat_1.
PFam; PF00014; Kunitz_BPTI; 10.
PFam; PF00086; thryroglobulin_1; 1.
BINTS; PR00759; BASICPTASE.
PRODOM; PD000222; Kunitz_BPTI; 10.
SMART; SM0131; KU; 10.
SMART; SM00211; TY; 1.
SMART; SM00289; WR1; 4.
PROSITE; PS00280; BPTI_KUNITZ_1; 8.
PROSITE; PS50279; BPTI_KUNITZ_2; 10.
PROSITE; PS00484; THYROGLOBULIN_1; 1.
Protease inhibitor; Serine protease inhibitor.
SEQUENCE 2225 AA; 242198 MW; A5DD8AE9D2A7B02A CRC64;

Query Match 74.5%; Score 35; DB 5; Length 2225;
1st Local Similarity 60.0%; Pred. No. 33;
Itches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
1 GPCXXXFIRY 10
470 GPCHGGSFQRY 479

JLT 9
[74] Q19474 PRELIMINARY; PRT; 91 AA.
01-JAN-1998 (TREMBLrel. 05, Created)
01-JAN-1998 (TREMBLrel. 05, Last sequence update)
01-JUN-2003 (TREMBLrel. 24, Last annotation update)
MHC class I c5/g1 (rla) (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
MEDLINE=85206117; PubMed=3997208;
Rogers J.H.; "Family organization of mouse H-2 class I genes.";
Immunogenetics 21:343-353(1985).
EMBL; M14828; AAA39688.1; -.
PIR; I68704; I68704.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR001039; MHC_I.
PFam; PF00129; MHC_I; 1.
PRINTS; PR01638; MHCLASSI.
PRODOM; PD000050; MHC_I; 1.
NON_TER 1 1
SEQUENCE 91 AA; 10671 MW; 4A5571396359B05F CRC64;

Query Match 72.3%; Score 34; DB 7; Length 91;
1st Local Similarity 50.0%; Pred. No. 2.8;
Itches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 GPCXXXFIRY 10
1 GPCKDKSSLRY 80

RESULT 10
Q8NAK6 PRELIMINARY; PRT; 224 AA.
ID Q8NAK6
AC Q8NAK6;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ35180.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
TISSUE=Placenta;
RC Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R., RA
RA Otsubi T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., RA
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., RA
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., RA
RA Murakawa K., Kanehori K., Takahashi-Fuji A., Oshima A., Suzuki Y., RA
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; RT
RT "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK092499; BAC03906.1; DR
GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR008296; TFPI.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR PRINTS; PRO0759; BASICPTASE.
DR PRODom; PD000222; Kunitz_BPTI; 3.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS000280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 3.
DR PIRSF; PIRSF001620; TFPI; 1.
DR Hypothetical protein; Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 224 AA; 25795 MW; F586328C31344765 CRC64;

Query Match 72.3%; Score 34; DB 4; Length 224;
Best Local Similarity 50.0%; Pred. No. 6.5%;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 GPCXXXFIRY 10
Db 1 GPCXXXFIRY 10
32 GPCRALLRY 41

RESULT 11
Q62323 PRELIMINARY; PRT; 253 AA.
ID Q62323
AC Q62323;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE TL antigen (Fragment).
GN H2-T18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=8610114; PubMed=3840195;
RA Chen Y.T., Obata Y., Stockert E., Old L.J.; RT "Thymus-leukemia (rl) antigens of the mouse.";
RL J. Exp. Med. 162:1134-1148(1985); CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).
CC DR EMBL; X03052; CAA26860.1; DR
PIR; I48850; I48850.
DR HSSP; P01901; 1BQH.
DR MGD; MGI:95950; H2-T18.

DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR PRINTS; PR01638; MHCLASSI.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IgC1; 1.
 DR PROSITE; PS50835; Ig_LIKE; 1.
 DR PROSITE; PS00290; Ig_MHC; 1.
 KW Glycoprotein; Transmembrane.
 PT NON_TER 1 1
 SQ SEQUENCE 253 AA; 28532 MW; SD001281SEC77FB1 CRC64;
 Query Match 72.3%; Score 34; DB 11; Length 253;
 Best Local Similarity 50.0%; Pred. No. 7.3;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 GPCXXXFIRY 10
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 57 GPCKDSLLRY 66
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RESULT 13
 ID Q860A1 PRELIMINARY;
 AC Q860A1;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE MHC class I antigen (Fragment).
 GN MUABTL.
 OS Mus abbotti (Abbott's mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TAXID=10108;
 RN [1]
 SEQUENCE FROM N.A.
 STRAIN=wild; TISSUE=Tail;
 MEDLINE=22359207; PubMed=12471122;
 RA Davis B.K., Cook R.G., Rich R.R., Rodgers J.R.;
 RT "Hyperconservation of the putative antigen recognition site of the MHC class I-b molecule TL in the subfamily Murinae: evidence that thymus leukemia antigen is an ancient mammalian gene.";
 RT J. Immunol. 169:6890-6899(2002).
 RL EMBL; AY144133; AAP23909.1;
 DR EMBL; AY144132; AAP23909.1; JOINED.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR00345; Cytc heme_BS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PB00129; MHC_I; 1.
 DR PRINTS; PRO1638; MHCLASSI.
 DR PRODOM; PD000050; MHC_I; 1.
 DR SMART; SM00407; IgC1; 1.
 DR PROSITE; PS50835; Ig_LIKE; 1.
 DR PROSITE; PS00290; Ig_MHC; 1.
 FT NON_TER 1 1
 FT NON_TER 272 272
 SQ SEQUENCE 272 AA; 31380 MW; C8E5D1FD7028AB1A CRC64;
 Query Match 72.3%; Score 34; DB 7; Length 272;
 Best Local Similarity 50.0%; Pred. No. 7.8;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 GPCXXXFIRY 10
 |||| :|||
 Db 160 GPCKDSLLRY 169

RESULT 14
 ID Q85ZZ9 PRELIMINARY;
 AC Q85ZZ9;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE MHC class I antigen (Fragment).
 GN MUATL.
 OS Mus caroli (Wild mouse) (Ricefield mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TAXID=10089;
 RN [1]
 SEQUENCE FROM N.A.
 TISSUE=Tail;
 MEDLINE=22359207; PubMed=12471122;
 RA Davis B.K., Cook R.G., Rich R.R., Rodgers J.R.;
 RT "Hyperconservation of the putative antigen recognition site of the MHC class I-b molecule TL in the subfamily Murinae: evidence that thymus leukemia antigen is an ancient mammalian gene.";
 RT J. Immunol. 169:6890-6899(2002).
 RL EMBL; AY144137; AAP23911.1;
 DR InterPro; IAY144136; AAP23911.1; JOINED.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PB00129; MHC_I; 1.
 DR PRINTS; PRO1638; MHCLASSI.
 DR PRODom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IgC1; 1.
 DR PROSITE; PS50835; Ig_LIKE; 1.
 DR PROSITE; PS00290; Ig_MHC; 1.
 FT NON_TER 1 1
 FT NON_TER 272 272
 SQ SEQUENCE 272 AA; 31647 MW; DFB1FFBAFFDDPCB59 CRC64;
 Query Match 72.3%; Score 34; DB 7; Length 272;
 Best Local Similarity 50.0%; Pred. No. 7.8;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 GPCXXXFIRY 10
 |||| :|||

MEDLINE=22359207; PubMed=12471122;
 Davis B.K., Cook R.G., Rich R.R., Rodgers J.R.;
 "Hyperconservation of the putative antigen recognition site of the MHC
 Class I-b molecule T_L in the subfamily Murinae: evidence that thymus
 leukemia antigen is an ancient mammalian gene.",
J. Immunol. 169: 6890-6899 (2002).

EMBL; AY144139; AAP23912.1; -.
 EMBL; AY144138; AAP23912.1; JOINED.
 GO; GO:0016020; C:membrane; IEA.
 GO; GO:0006955; P:immune response; IEA.
 InterPro; IPR007110; Ig-like.
 InterPro; IPR003597; Ig_C1.
 InterPro; IPR003006; Ig_MHC.
 InterPro; IPR001039; MHC_I.
 Pfam; PF00047; Ig; 1.
 Pfam; PF00129; MHC_I; 1.
 PRINTS; PRO1638; MHCLASSI.
 PRODom; PD000050; MHC_I; 1.
 SMART; SM00407; IGG1; 1.
 PROSITE; PS50835; IG_LIKE; 1.
 PROSITE; PS00290; Ig_MHC; 1.
 NON_TER 1 272
 NON_TER 272 272
 SEQUENCE 272 AA; 31592 MW; 2FB1FFBCFDD5914 CRC64;

Query Match 72.3%; Score 34; DB 7; Length 272;
 Best Local Similarity 50.0%; Pred. No. 7.8;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 SMART 1 272
 SMART 1 272
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 PROSITE 1 272
 NON_TER 1 272
 NON_TER 272 272
 SEQUENCE 272 AA; 31592 MW; 2FB1FFBCFDD5914 CRC64;

JLT 15

Q85ZZZ6 PRELIMINARY; PRT; 272 AA.

Q85ZZZ6; 01-JUN-2003 (TREMBLrel. 24, Created)
 01-OCT-2003 (TREMBLrel. 24, Last sequence update)
 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 MHC class I antigen (Fragment).
 MPUTL.

Mus dunni (Pygmy mouse) (*Mus* *terricolor*).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10110;
 [1]

SEQUENCE FROM N.A.

STRAIN=Wild; TISSUE=Tail;

MEDLINE=22359207; PubMed=12471122;

Davis B.K., Cook R.G., Rich R.R., Rodgers J.R.;
 "Hyperconservation of the putative antigen recognition site of the MHC
 Class I-b molecule T_L in the subfamily Murinae: evidence that thymus
 leukemia antigen is an ancient mammalian gene.",
J. Immunol. 169: 6890-6899 (2002).

EMBL; AY144145; AAP23915.1;
 EMBL; AY144144; AAP23915.1; JOINED.
 GO; GO:0016020; C:membrane; IEA.
 GO; GO:0005489; F:electron transporter activity; IEA.
 GO; GO:0006118; P:electron transport; IEA.
 GO; GO:0006955; P:immune response; IEA.
 InterPro; IPR000345; CytC_heme_BS.
 InterPro; IPR007110; Ig-like.

InterPro; IPR003597; Ig_C1.
 InterPro; IPR003006; Ig_MHC.
 InterPro; IPR001039; MHC_I.
 Pfam; PF00047; Ig; 1.
 Pfam; PF00129; MHC_I; 1.
 PRINTS; PRO1638; MHCLASSI.
 PRODom; PD000050; MHC_I; 1.
 SMART; SM00407; IGG1; 1.
 PROSITE; PS00190; CYTOCHROME_C; 1.

DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS00290; Ig_MHC; 1.
 FT NON_TER 1
 FT NON_TER 272
 SQ SEQUENCE 272 AA; 31489 MW; 0C8CB21EA4CD1F77 CRC64;

Query Match 72.3%; Score 34; DB 7; Length 272;
 Best Local Similarity 50.0%; Pred. No. 7.8;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 GPCXXXFIRY 10
 Db 160 GPCKDSSLRY 169

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GenCore version 5.1.6
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protein - protein search, using sw model

on: August 11, 2004, 13:00:42 ; Search time 50.2857 seconds
 (without alignments)
 61.807 Million cell updates/sec

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Searched: 1586107 seqs, 282547505 residues

All number of hits satisfying chosen parameters: 1586107

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Listing First 45 summaries

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ALIGNMENTS

26 44 88.0 75 2 AAW26361
 27 44 88.0 77 1 AAP94153
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 AapB0400 Human pan
 Aau97781 Human pan
 Aar65482 Fusion pr
 Aab54299 Human pan
 Abg27312 Novel hum
 Aar92296 PSKAN8 Pr
 Abg27311 Novel hum
 Abu09384 Consensus
 Abp57288 Kazal typ
 Abp57290 Kazal typ
 Abp57291 Kazal typ
 Aar43918 Mutant mo
 Aar43917 Mutant mo
 Aar35229 Monitor p
 Abp57286 Kazal typ
 Abp57287 Kazal typ
 AAP82622 Pancreati

RESULT 1

AAP90597
 ID AAP90597 standard; protein; 50 AA.
 XX AAP90597;
 AC XX DT 25-MAR-2003 (revised)
 DT 11-JUN-1989 (first entry)
 XX DE Sequence of human pancreatic secretory trypsin inhibitor (PSTI).
 XX KW Human pancreatic secretory trypsin inhibitor; PSTI.
 XX OS Homo sapiens.
 XX PN EP300459-A.
 XX PD 25-JAN-1989.
 XX PF 20-JUL-1988; 88EP-00111704.
 XX PR 23-JUL-1987; 87JP-00184556.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Alt No.	Score	Query Match	Length	DB	ID	Description
1	44	88.0	50	1	AAP90597	Aap90597 Sequence
2	44	88.0	55	1	AAP90596	Aap90596 Sequence
3	44	88.0	55	1	AAP90595	Aap90595 Sequence
4	44	88.0	56	1	AAP82648	Aap82648 Pancreati
5	44	88.0	56	1	AAP82613	Aap82613 Pancreati
6	44	88.0	56	1	AAP82650	Aap82650 Pancreati
7	44	88.0	56	1	AAP82649	Aap82649 Pancreati
8	44	88.0	56	1	AAP82653	Aap82653 Pancreati
9	44	88.0	56	1	AAP82611	Aap82611 Pancreati
10	44	88.0	56	1	AAP82618	Aap82618 Pancreati
11	44	88.0	56	1	AAP82652	Aap82652 Pancreati
12	44	88.0	56	1	AAP82651	Aap82651 Pancreati
13	44	88.0	56	1	AAP82612	Aap82612 Pancreati
14	44	88.0	56	1	AAP82623	Aap82623 Pancreati
15	44	88.0	56	1	AAP80003	Aap80003 Pancreati
16	44	88.0	56	1	AAP90594	Aap90594 Sequence
17	44	88.0	56	2	AAR14631	Aar14631 Pancreas
18	44	88.0	56	2	AAR14632	Aar14632 Pancreas
19	44	88.0	56	2	AAR22622	Aar22622 PTSI enco
20	44	88.0	57	1	AAP81182	Aap81182 Human pan
21	44	88.0	57	1	AAP94152	Aap94152 Sequence
22	44	88.0	57	2	AAR03728	Aar03728 Modified
23	44	88.0	57	2	AAR03727	Aar03727 Modified
24	44	88.0	57	2	AAR14629	Aar14629 Pancreas
25	44	88.0	57	2	AAR14629	Aar14629

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 Best Local Similarity 70.0%; Pred. No. 0.57;
 Matches 7; Conservative 0; Mismatches 3;
 Indels 0; Gaps 0;

WPI; 1988-192315/28.
N-PSDB; AAN82228.

Analogues of pancreatic secretory trypsin inhibitor - are protease inhibitors with high specificity for leukocyte elastase.

Claim 8; Page 62; 74pp; English.

The protein was produced from a DNA sequence constructed from 25 oligonucleotides and is one of 24 analogues of PSTI. A master gene, encoding PSTI 0, (having essentially the same sequence as reported by L.J. Greene, 1976, Methods Enzymol. 45, 813-825) was used as a template for the construction of novel genes. See also AAP82611-23 and AAP82649-54. (Updated on 25-MAR-2003 to correct PI field.)

Sequence 56 AA;

Query Match	88.0%	Score 44;	DB 1;	Length 56;
Best Local Similarity	70.0%	Pred. No. 0.63;		
Matches	7;	Conservative	0;	Gaps 0;

2 GCXXIYXPVC 11
15 GCTIYNPVC 24

JLT 5
12613
AAP82613 standard; protein; 56 AA.

13-JUL-1988.

25-MAR-2003 (revised)

06-NOV-1990 (first entry)

Pancreatic secretory trypsin inhibitor, PSTI 3 (Tyr18, Glu19, Arg21).
PSTI 3; pancreatic secretory trypsin inhibitor; protease;
leukocyte elastase.

Synthetic.

Key
Misc-difference 18
/label= site-directed mutn.
/note= "Lys>Tyr"

Misc-difference 19
/label= site-directed mutn.
/note= "Ile>Glu"

Misc-difference 21
/label= site-directed mutn.
/note= "Asn>Arg"

GB2199582-A.

13-JUL-1988.

07-JAN-1987; 87GB-00000204.

07-JAN-1987; 87GB-00000204.

(FARB) BAYER AG.

Collins D, Blocker H, Frank R, Maywald F, Fritz H, Bruns W;

13-JUL-1988.

07-JAN-1987; 87GB-00000204.

07-JAN-1987; 87GB-00000204.

(FARB) BAYER AG.

Collins D, Blocker H, Frank R, Maywald F, Fritz H, Bruns W;

WPI; 1988-192315/28.

N-PSDB; AAN82218.

Analogues of pancreatic secretory trypsin inhibitor - are protease inhibitors with high specificity for leukocyte elastase.

Claim 8; Page 62; 74pp; English.

XX

The protein was produced from a DNA sequence constructed from 25 oligonucleotides and is one of 24 analogues of PSTI. A master gene, encoding PSTI 0, (having essentially the same sequence as reported by L.J. Greene, 1976, Methods Enzymol. 45, 813-825) was used as a template for the construction of novel genes. See also AAP82611-23 and AAP82649-54. (Updated on 25-MAR-2003 to correct PI field.)

XX

SQ Sequence 56 AA;

Query Match	88.0%	Score 44;	DB 1;	Length 56;
Best Local Similarity	70.0%	Pred. No. 0.63;		
Matches	7;	Conservative	0;	Gaps 0;

Qy 2 GCXXIYXPVC 11
15 GCTIYNPVC 24

Db

RESULT 6				
ID AAP82650	ID AAP82650 standard; protein; 56 AA.			
XX	XX			
AC	AC			
XX	XX			
DT	DT 25-MAR-2003 (revised)			
DT	DT 06-NOV-1990 (first entry)			
XX	XX	Pancreatic secretory trypsin inhibitor, PSTI 20 (Ile18, Asp21, Asn29).		
DE	DE	Pancreatic secretory trypsin inhibitor; protease;		
XX	XX	PSTI 20; Pancreatic secretory trypsin inhibitor; protease;		
KW	KW leukocyte elastase.			
XX	XX			
OS	OS Synthetic.			
XX	XX			
FH	FH Key			
FT	FT Misc-difference 18	/label= site-directed mutn.		
FT	FT /note= "Lys>Val"			
FT	FT Misc-difference 21	/label= site-directed mutn.		
FT	FT /note= "Asn>Asp"			
FT	FT Misc-difference 29	/label= site-directed mutn.		
FT	FT /note= "Asp>Asn"			
XX	XX			
PN	PN GB2199582-A.			
XX	XX			
PD	PD 13-JUL-1988.			
XX	XX			
PF	PF 07-JAN-1987; 87GB-00000204.			
XX	XX			
PR	PR 07-JAN-1987; 87GB-00000204.			
XX	XX			
PA	PA (FARB) BAYER AG.			
XX	XX			
PI	PI Collins D, Blocker H, Frank R, Maywald F, Fritz H, Bruns W;			
XX	XX			
DR	DR WPI; 1988-192315/28.			
DR	DR N-PSDB; AAN82230.			
XX	XX			
PT	PT Analogues of pancreatic secretory trypsin inhibitor - are protease			
PT	PT inhibitors with high specificity for leukocyte elastase.			
XX	XX			
PS	PS Claim 8; Page 62; 74pp; English.			
XX	XX			

The protein was produced from a DNA sequence constructed from 25 oligonucleotides and is one of 24 analogues of PSTI. A master gene, encoding PSTI 0, (having essentially the same sequence as reported by L.J. Greene, 1976, Methods Enzymol. 45, 813-825) was used as a template for the construction of novel genes. See also AAP82611-23 and AAP82649-54. (Updated on 25-MAR-2003 to correct PI field.)

XX

SO Sequence 56 AA;

Query Match 88.0%; Score 44; DB 1; Length 56;
Best Local Similarity 70.0%; Pred. No. 0.63;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 7
ID AAP82649
ID AAP82649 standard; protein; 56 AA.

Qy 2 GCXXIYXPVC 11
| | |||
Db 15 GCTIYDPVC 24

RESULT 8
ID AAP82653
ID AAP82653 standard; protein; 56 AA.

XX
AC AAP82653;
XX
XX DT 25-MAR-2003 (revised)
DT 06-NOV-1990. (First entry)

XX DE Pancreatic secretory trypsin inhibitor, PSTI 23 (Phe18).

XX KW PSTI 23; pancreatic secretory trypsin inhibitor; protease;
KW leukocyte elastase.

XX OS synthetic.

XX FH Key
FT Misc-difference 18
FT /label= Site-directed mutn.
FT /note= "Lys>Phe"

XX FT Location/Qualifiers
Key
FT Misc-difference 18
FT /label= site-directed mutn.
FT /note= "Lys>Val"

XX FT Location/Qualifiers
Key
FT Misc-difference 21
FT /label= site-directed mutn.
FT /note= "Asn>Asp"

XX FT Location/Qualifiers
Key
FT Misc-difference 29
FT /label= site-directed mutn.
FT /note= "Asp>Asn"

XX PN GB2199582-A.

XX PD 13-JUL-1988.

XX PP 07-JAN-1987; 87GB-00000204.

XX PR 07-JAN-1987; 87GB-00000204.

XX PA (FARB) BAYER AG.

XX PI Collins D, Blocker H, Frank R, Maywald F, Fritz H, Bruns W;

XX DR WPI; 1988-192315/28.
DR N-PSDB; AAN82233.

XX PT Analogues of pancreatic secretory trypsin inhibitor - are protease
inhibitors with high specificity for leukocyte elastase.

XX PS Claim 8; Page 62; 74pp; English.

XX PS Claim 8; Page 62; 74pp; English.

XX PR 07-JAN-1987; 87GB-00000204.

XX PR 07-JAN-1987; 87GB-00000204.

XX PA (FARB) BAYER AG.

XX PI Collins D, Blocker H, Frank R, Maywald F, Fritz H, Bruns W;

XX DR WPI; 1988-192315/28.
DR N-PSDB; AAN82229.

XX PT Analogues of pancreatic secretory trypsin inhibitor - are protease
inhibitors with high specificity for leukocyte elastase.

XX PS Claim 8; Page 62; 74pp; English.

XX CC The protein was produced from a DNA sequence constructed from 25
CC oligonucleotides and is one of 24 analogues of PSTI. A master gene,
CC encoding PSTI 0, (having essentially the same sequence as reported by
CC L.J. Greene, 1976, Methods Enzymol. 45, 813-825) was used as a template
CC for the construction of novel genes. See also AAP82611-23 and AAP82648-
CC 54. (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 56 AA;

Query Match 88.0%; Score 44; DB 1; Length 56;
Best Local Similarity 70.0%; Pred. No. 0.63;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCXXIYXPVC 11
| | |||

RESULT 9
ID AAP82611
ID AAP82611 standard; protein; 56 AA.

XX AC AAP82611;

XX DT 06-NOV-1990 (First entry)

XX DE Pancreatic secretory trypsin inhibitor, PSTI 1 (Leu18).

XX KW PSTI 1; pancreatic secretory trypsin inhibitor; protease;

leukocyte elastase.

Synthetic.

Key Location/Qualifiers
Misc-difference 18
 /label= "site-directed mutn.
 /note= "Lys>Leu"

GB2199582-A.

13-JUL-1988.

07-JAN-1987; 87GB-00000204.

07-JAN-1987; 87GB-00000204.

(FARB) BAYER AG.

Collins D, Blocker H, Frank R, Maywald F, Fritz H, Bruns W;
 WPI; 1988-192315/28.
 N-PSDB; AAN82216.

Analogues of pancreatic secretory trypsin inhibitor - are protease inhibitors with high specificity for leukocyte elastase.

Claim 8; Page 62; 74pp; English.

The protein was produced from a DNA sequence constructed from 25 oligonucleotides and is one of 24 analogues of PSTI. A master gene, encoding PSTI 0, (having essentially the same sequence as reported by L.J. Greene, 1976, Methods Enzymol. 45, 813-825) was used as a template for the construction of novel genes. See also AAP82611-23 and AAP82648-54. (Updated on 25-MAR-2003 to correct PI field.)

Sequence 56 AA;

Query	Match	88.0%; Score 44; DB 1; Length 56;
	Best Local Similarity	70.0%; Pred. No. 0.63;
	Matches	0; Mismatches 0; Indels 0; Gaps 0;

Sequence 56 AA;

Query	Match	88.0%; Score 44; DB 1; Length 56;
	Best Local Similarity	70.0%; Pred. No. 0.63;
	Matches	0; Mismatches 0; Indels 0; Gaps 0;

JLT 10
 32618
 AAP82618 standard; protein; 56 AA.

AAP82618;

25-MAR-2003 *(revised)*
 06-NOV-1990 *(first entry)*

Pancreatic secretory trypsin inhibitor, PSTI 7 (Leu18,Arg21).

PSTI 7; pancreatic secretory trypsin inhibitor; protease;
 leukocyte elastase.

Synthetic.

Key Location/Qualifiers
Misc-difference 18
 /label= site-directed mutn.
 /note= "Lys>Leu"
Misc-difference 21
 /label= site-directed mutn.
 /note= "Asn>Arg"

GB2199582-A.

13-JUL-1988.

XX PF 07-JAN-1987; 87GB-00000204.
 XX PR 07-JAN-1987; 87GB-00000204.
 XX PA (FARB) BAYER AG.
 XX PI Collins D, Blocker H, Frank R, Maywald F, Fritz H, Bruns W;
 XX DR 1988-192315/28.
 XX DR N-PSDB; AAN82222.

Analogues of pancreatic secretory trypsin inhibitor - are protease inhibitors with high specificity for leukocyte elastase.

Claim 8; Page 62; 74pp; English.

The protein was produced from a DNA sequence constructed from 25 oligonucleotides and is one of 24 analogues of PSTI. A master gene, encoding PSTI 0, (having essentially the same sequence as reported by L.J. Greene, 1976, Methods Enzymol. 45, 813-825) was used as a template for the construction of novel genes. See also AAP82611-23 and AAP82648-54. (Updated on 25-MAR-2003 to correct PI field.)

Sequence 56 AA;

Query	Match	88.0%; Score 44; DB 1; Length 56;
	Best Local Similarity	70.0%; Pred. No. 0.63;
	Matches	0; Mismatches 0; Indels 0; Gaps 0;

Query	Match	88.0%; Score 44; DB 1; Length 56;
	Best Local Similarity	70.0%; Pred. No. 0.63;
	Matches	0; Mismatches 0; Indels 0; Gaps 0;

Sequence 56 AA;

Query	Match	88.0%; Score 44; DB 1; Length 56;
	Best Local Similarity	70.0%; Pred. No. 0.63;
	Matches	0; Mismatches 0; Indels 0; Gaps 0;

Pancreatic secretory trypsin inhibitor, PSTI 22 (Tyr18).

PSTI 22; pancreatic secretory trypsin inhibitor; protease;
 leukocyte elastase.

Sequence 56 AA;

Query	Match	88.0%; Score 44; DB 1; Length 56;
	Best Local Similarity	70.0%; Pred. No. 0.63;
	Matches	0; Mismatches 0; Indels 0; Gaps 0;

Pancreatic secretory trypsin inhibitor, PSTI 22 (Tyr18).

Synthetic.

Key Location/Qualifiers
Misc-difference 18
 /label= "Lys>Tyr"
 /note= "Lys>Tyr"

XX PR 07-JAN-1987; 87GB-00000204.
 XX PA (FARB) BAYER AG.
 XX PI Collins D, Blocker H, Frank R, Maywald F, Fritz H, Bruns W;
 XX DR 1988-192315/28.
 XX DR N-PSDB; AAN82232.

Analogues of pancreatic secretory trypsin inhibitor - are protease inhibitors with high specificity for leukocyte elastase.

XX Claim 8; Page 62; 74pp; English.

XX The protein was produced from a DNA sequence constructed from 25 oligonucleotides and is one of 24 analogues of PSTI. A master gene, encoding PSTI 0, (having essentially the same sequence as reported by L.J. Greene, 1976, Methods Enzymol. 45, 813-825) was used as a template for the construction of novel genes. See also AAP82611-23 and AAP82648-54. (Updated on 25-MAR-2003 to correct PI field.)

SQ Sequence 56 AA;

```

Query Match          88.0%; Score 44; DB 1; Length 56;
Best Local Similarity 70.0%; Pred. No. 0.63;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

Qy 2 GCXXIYXPVC 11
Db 15 GCTLIYDPVC 24

RESULT 12
ID AAP82651 standard; protein; 56 AA.
AC AAP82651;
XX DT 25-MAR-2003 (revised)
DT 06-NOV-1990 (first entry)
DE Pancreatic secretory trypsin inhibitor, PSTI 2 (Leu18,Asp21,Asn29).
XX KW PSTI 2; pancreatic secretory trypsin inhibitor; protease;
KW leukocyte elastase.
XX OS synthetic.
XX FH Key Location/Qualifiers
FT Misc-difference 18
FT /label= site-directed mutn.
FT /note= "Lys>Leu"
FT Misc-difference 21
FT /label= site-directed mutn.
FT /note= "Asn>Asp"
FT Misc_difference 29
FT /label= site-directed mutn.
FT /note= "Asp>Asn"
XX PN GB2199582-A.
XX PD 13-JUL-1988.
XX PF 07-JAN-1987; 87GB-00000204.
XX PR 07-JAN-1987; 87GB-00000204.
XX PA (FARB) BAYER AG.
XX PI Collins D, Blocker H, Frank R, Maywald F, Fritz H, Bruns W;
XX DR WPI; 1988-192315/28.
XX DR N-PSDB; AAN82231.
XX PP 07-JAN-1987; 87GB-00000204.
XX PR 07-JAN-1987; 87GB-00000204.
XX PA (FARB) BAYER AG.
XX PI Collins D, Blocker H, Frank R, Maywald F, Fritz H, Bruns W;
XX DR WPI; 1988-192315/28.
XX DR N-PSDB; AAN82231.
XX PT Analogues of pancreatic secretory trypsin inhibitor - are protease inhibitors with high specificity for leukocyte elastase.
XX PT claim 8; Page 62; 74pp; English.
XX SQ Sequence 56 AA;

CC 54. (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 56 AA;

```

Query Match          88.0%; Score 44; DB 1; Length 56;
Best Local Similarity 70.0%; Pred. No. 0.63;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

Qy 2 GCXXIYXPVC 11
Db 15 GCTLIYDPVC 24

RESULT 13
ID AAP82612 standard; protein; 56 AA.
XX AC AAP82612;
XX DT 25-MAR-2003 (revised)
DT 06-NOV-1990 (first entry)
XX DE Pancreatic secretory trypsin inhibitor, PSTI 2 (Leu18,Asp21,Asn29).
XX KW PSTI 2; pancreatic secretory trypsin inhibitor; protease;
KW leukocyte elastase.
XX OS synthetic.
XX FH Key Location/Qualifiers
FT Misc-difference 18
FT /label= site-directed mutn.
FT /note= "Lys>Leu"
FT Misc-difference 21
FT /label= site-directed mutn.
FT /note= "Asn>Asp"
FT Misc_difference 29
FT /label= site-directed mutn.
FT /note= "Asp>Asn"
XX PN GB2199582-A.
XX PD 13-JUL-1988.
XX PF 07-JAN-1987; 87GB-00000204.
XX PR 07-JAN-1987; 87GB-00000204.
XX PA (FARB) BAYER AG.
XX PI Collins D, Blocker H, Frank R, Maywald F, Fritz H, Bruns W;
XX DR WPI; 1988-192315/28.
XX DR N-PSDB; AAN82217.
XX PT Analogues of pancreatic secretory trypsin inhibitor - are protease inhibitors with high specificity for leukocyte elastase.
XX PT claim 8; Page 62; 74pp; English.
XX SQ Sequence 56 AA;

CC The protein was produced from a DNA sequence constructed from 25 oligonucleotides and is one of 24 analogues of PSTI. A master gene, encoding PSTI 0, (having essentially the same sequence as reported by L.J. Greene, 1976, Methods Enzymol. 45, 813-825) was used as a template for the construction of novel genes. See also AAP82611-23 and AAP82648-54. (Updated on 25-MAR-2003 to correct PI field.)

CC Sequence 56 AA;

```

Query Match          88.0%; Score 44; DB 1; Length 56;
Best Local Similarity 70.0%; Pred. No. 0.63;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

CC The protein was produced from a DNA sequence constructed from 25 oligonucleotides and is one of 24 analogues of PSTI. A master gene, encoding PSTI 0, (having essentially the same sequence as reported by L.J. Greene, 1976, Methods Enzymol. 45, 813-825) was used as a template for the construction of novel genes. See also AAP82611-23 and AAP82648-54. (Updated on 25-MAR-2003 to correct PI field.)

2 GCXXIYXPVC 11
 | | ||||
 15 GCTLIYDPVC 24

JLT 14
 12623 AAP82623 standard; protein; 56 AA.

AAP82623;
 25-MAR-2003 (revised)
 06-NOV-1990 (first entry)

Pancreatic secretory trypsin inhibitor, PSTI 17 (Val18).
 PSTI 17; pancreatic secretory trypsin inhibitor; protease;
 leukocyte elastase.
 Synthetic.

Key Location/Qualifiers
 Misc-difference 18
 /label= site-directed mutn.
 /note= "Lys>Val"

GB2199582-A.
 13-JUL-1988.
 07-JAN-1987; 87GB-00000204.
 07-JAN-1987; 87GB-00000204.
 (FARB) BAYER AG.

Collins D, Blocker H, Frank R, Maywald F, Fritz H, Bruns W;
 WPI; 1988-192315/28.
 N-PSDB; AANB0030.

Analogues of pancreatic secretory trypsin inhibitor - are protease
 inhibitors with high specificity for leukocyte elastase.

Claim 8; Page 62; 74pp; English.

The protein was produced from a DNA sequence constructed from 25
 Oligonucleotides and is one of 24 analogues of PSTI. A master gene,
 encoding PSTI 0, (having essentially the same sequence as reported by
 L.J. Greene, 1976, Methods Enzymol. 45, 813-825) was used as a template
 for the construction of novel genes. See also AAP82611-23 and AAP82648-
 54. (Updated on 25-MAR-2003 to correct PI field.)

Sequence 56 AA;

Query Match 88.0%; Score 44; DB 1; Length 56;
 1st Local Similarity 70.0%; Pred. No. 0.63;
 itches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 2 GCXXIYXPVC 11
 15 GCTVIYNPVC 24

JLT 15
 10003 AAP80003 standard; protein; 56 AA.
 AAP80003;
 06-NOV-1990 (first entry)

Pancreatic secretory trypsin inhibitor, PSTI 0.

XX PSTI 0; pancreatic secretory trypsin inhibitor; protease;
 KW
 KW leukocyte elastase.
 XX
 OS Synthetic.
 XX
 PN GB2199582-A.
 XX
 PD 13-JUL-1988.
 XX
 PF 07-JAN-1987; 87GB-00000204.
 XX
 PR 07-JAN-1987; 87GB-00000204.
 XX
 PA (FARB) BAYER AG.

Collins D, Blocker H, Frank R, Maywald F, Fritz H, Bruns W;
 WPI; 1988-192315/28.
 DR
 DR N-PSDB; AANB0030.

Analogue of pancreatic secretory trypsin inhibitor - are protease
 PT inhibitors with high specificity for leukocyte elastase.
 XX
 Disclosure; Page ? ; 74pp; English.

The protein was produced from a DNA sequence constructed from 25
 oligonucleotides and has the same sequence as the natural PSTI 0. A
 master gene, encoding PSTI 0, (having essentially the same sequence as
 reported by L.J. Greene, 1976, Methods Enzymol. 45, 813-825) was used as
 a template for the construction of novel genes. See also AAP82611-23 and
 AAP82648-54

XX
 SQ Sequence 56 AA;

Query	Match	88.0%	Score	44	DB	1	Length	56
	Best Local Similarity	70.0%	Pred. No.	0.63				
	Matches	7	Mismatches	3	Indels	0	Gaps	0

Qy 2 GCXXIYXPVC 11
 Db 15 GCTVIYNPVC 24

Search completed: August 11, 2004, 13:07:40
 Job time : 51.2857 secs

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protein - protein search, using sw model

on: August 11, 2004, 13:04:58 ; Search time 12.0476 Seconds
 (without alignments)
 87.827 Million cell updates/sec

le: US-10-661-207-2
 Effect score: 50
 Sequence: 1 XGCXXIYXPVC 11

Ring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

11 number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

: Processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : PIR78:
 1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Alt No.	Score	Query	Match	Length	DB ID	Description
1	44	88.0	79	1	TIHUA	pancreatic secretory trypsin inhibitor precursor
2	42	84.0	56	1	TIBOA	pancreatic secretory trypsin inhibitor precursor
3	42	84.0	56	1	TISHA	pancreatic secretory trypsin inhibitor precursor
4	42	84.0	56	1	TIPG	pancreatic secretory trypsin inhibitor precursor
5	42	84.0	57	1	TIDGA	pancreatic secretory trypsin inhibitor precursor
6	42	84.0	79	1	TIRT1	pancreatic secretory trypsin inhibitor precursor
7	42	84.0	80	1	S01498	peptide PEC-60 precursor
8	38	76.0	86	1	A34427	ovoinhibitor precursor
9	38	76.0	472	1	A26730	agrin - rat
10	38	76.0	1959	1	AGR1	ovomucoid, third domain
11	37	74.0	53	2	G31438	voltage-gated sodium channel protein
12	36	72.0	1699	2	T31340	pancreatic secretory trypsin inhibitor precursor
13	35	70.0	79	1	TIRT2	hypothetical protein
14	35	70.0	93	2	JA0128	diacylglycerol kinase
15	35	70.0	1154	2	T18525	nucleic acid-binding protein
16	34	68.0	94	1	B48549	ecdysone-inducible protein
17	34	68.0	341	2	A48422	hypothetical protein
18	34	68.0	746	2	G84605	ovomucoid, third domain
19	33	66.0	54	2	H31444	hypothetical protein
20	33	66.0	772	2	H84605	hypothetical protein
21	33	66.0	802	2	B84560	fatty-acid synthase
22	33	66.0	2422	2	T18201	hypothetical protein
23	32	64.0	128	2	A29349	receptor-like protein
24	32	64.0	201	2	C85253	receptor-like protein
25	32	64.0	201	2	T49121	thymidine kinase U
26	32	64.0	223	2	F82870	hypothetical protein
27	32	64.0	572	2	T16865	hypothetical protein
28	32	64.0	609	2	T25120	hypothetical protein
29	32	64.0	727	2	S42834	F40F12.5 protein

RESULT 1

TIHUA

pancreatic secretory trypsin inhibitor precursor [validated] - human
 N; Alternate names: endothelial cell growth factor 2a

C; Species: Homo sapiens (man)

C; Date: 30-Nov-1980 #sequence revision 17-Feb-1994 #text change 08-Dec-2000

C; Accession: A27484; S02605; A90062; A92355; A255604; 152210; A01229

R; Horii, A.; Kobayashi, T.; Tomita, N.; Yamamoto, T.; Murotsu, T.; Ogawa, A.; Biochem. Biophys. Res. Commun. 149, 635-641, 1987

A; Title: Primary structure of human pancreatic secretory trypsin inhibitor (PSTI) gene.
 A; Reference number: A27484; MUID:88106485; PMID:3501289

A; Accession: A27484

A; Molecule type: DNA

A; Residues: 1-79 <HOR>

A; Cross-references: GB:M20530; GB:M18374; NID:9190692; PID:AAA36522.1; PID:g190694

R; Tomita, N.; Horii, A.; Ogawa, M.; Mori, T.; Matsubara, K.

FEBS Lett. 225, 113-119, 1987

A; Title: Expression of pancreatic secretory trypsin inhibitor gene in neoplastic tissues
 A; Reference number: S02605; MUID:88083571; PMID:2961612

A; Accession: S02605

A; Molecule type: mRNA
 A; Residues: 1-63, 'G', 65-79 <TOM>

A; Cross-references: EMBL:Y00705; NID:935765; PID:CAA68697.1; PID:935766

A; Note: the authors translated the codon TAC for residue 33 as Thr and GGT for residue 64

R; Bartelt, D.C.; Shapanka, R.; Greene, L.J.

Arch. Biochem. Biophys. 179, 189-199, 1977

A; Title: The primary structure of the human pancreatic secretory trypsin inhibitor. Amino acid sequence of the protein
 A; Reference number: A90062; MUID:77133145; PMID:77133145

A; Accession: A90062

A; Molecule type: protein
 A; Residues: 24-43, 'N', 45-51, 'D', 53-79 <BAR>

A; Note: the inhibitor is present in multiple chromatographic forms differing in asparagine

R; Huhtala, M.L.; Pesonen, K.; Kalkkinen, N.; Stenman, U.H.

J. Biol. Chem. 257, 13713-13716, 1982

A; Title: Purification and characterization of a tumor-associated trypsin inhibitor from t
 A; Reference number: A92355; MUID:83056875; PMID:7142173

A; Accession: A92355

A; Molecule type: protein
 A; Residues: 24-31, 'X', 33-38, 'X', 40-43, 'N', 45-46 <HUX>

A; Note: this peptide was isolated from the urine of a patient with ovarian cancer

R; McKeehan, W.L.; Sakagami, Y.; Hoshi, H.; McKeehan, K.A.

J. Biol. Chem. 261, 5378-5383, 1986

A; Title: Two apparent human endothelial cell growth factors from human hepatoma cells are
 A; Reference number: A92583; MUID:8616B278; PMID:3007499

A; Accession: A26604

A; Molecule type: protein
 A; Residues: 24-31, 'X', 33-38, 'X', 40-46, 'X', 48 <MCX>

R; Yamamoto, T.; Nakamura, Y.; Nishide, T.; Mori, T.; Matsubara, K.

Biochem. Biophys. Res. Commun. 132, 605-612, 1985

A; Title: Molecular cloning and nucleotide sequence of human pancreatic secretory trypsin

A; Reference number: I52210; MUID:86050645; PMID:3877508

A; Accession: I52210

ALIGNMENTS

A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-79 <RES>
 C;Cross-references: GB: M11949; NID: g190687; PID: g190688
 C;Genetics:
 A;Gene: GDB: SPINK1
 A;Cross-references: GDB: 120383; OMIM: 167790
 A;Map position: 5q31-5q33
 A;Introns: 19/1; 29/3; 65/2
 C;Superfamily: pancreatic secretory trypsin inhibitor; Kazal proteinase inhibitor homolog
 C;Keywords: monomer; pancreas; serine protease inhibitor
 F;1-23/Domain: signal sequence #status predicted <SIG>
 F;24-79/Product: pancreatic secretory trypsin inhibitor #status experimental <MAT>
 F;30-79/Domain: Kazal proteinase inhibitor homology <KPI>
 F;32-61,39-58,47-79/Disulfide bonds: #status predicted
 P;41/Inhibitory site: Lys (trypsin) #status predicted

Query Match 88.0%; Score 44; DB 1; Length 79;
 Best Local Similarity 70.0%; Pred. No. 0.11;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 2
 TIBOA
 pancreatic secretory trypsin inhibitor - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 16-Jul-1999
 C;Accession: A01230
 R;Greene, L.J.; Bartelt, D.C.
 J. Biol. Chem. 244, 2646-2657, 1969
 A;Title: The structure of the bovine pancreatic secretory trypsin inhibitor - Kazal's inhibitor
 A;Reference number: A92046; MUID: 69187206; PMID: 5769997
 A;Accession: A01230
 A;Molecule type: protein
 A;Residues: 1-56 <GRE>
 R;Guy, O.; Shapanka, R.; Greene, L.J.
 J. Biol. Chem. 246, 7740-7747, 1971
 A;Title: The structure of the bovine pancreatic secretory trypsin inhibitor-Kazal's inhibitor
 A;Reference number: A92097; MUID: 72086018; PMID: 5135319
 A;Contents: annotation; disulfide bonds
 R;Rigbi, M.; Greene, L.J.
 J. Biol. Chem. 243, 5457-5464, 1968
 A;Title: Limited proteolysis of the bovine pancreatic secretory trypsin inhibitor at acidic pH
 A;Reference number: A92037; MUID: 69080142; PMID: 5750336
 A;Contents: annotation; inhibitory site
 C;Superfamily: pancreatic secretory trypsin inhibitor; Kazal proteinase inhibitor homolog
 C;Keywords: pancreas; serine proteinase inhibitor homology <KPI>
 F;7-56/Domain: Kazal proteinase inhibitor homology <KPI>
 F;9-38,16-35,24-56/Disulfide bonds: #status experimental
 P;18/Inhibitory site: Arg (trypsin) #status experimental

Query Match 84.0%; Score 42; DB 1; Length 56;
 Best Local Similarity 70.0%; Pred. No. 0.21;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 3
 TISHA
 pancreatic secretory trypsin inhibitor - sheep (tentative sequence)
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic Sheep)
 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
 C;Accession: A94487; A01230
 R;Tschesche, H.; Obermeier, R.; Hochstrasser, K.
 unpublished results, cited by Tschesche, H.; Wachter, E.; Kupfer, S.; Obermeier, R., Reijns, Fritz, H., and Tschesche, H., eds., pp. 207-222, Walter de Gruyter, New York

A;Reference number: A94487
 A;Accession: A94487
 A;Molecule type: protein
 A;Residues: 1-56 <TSC>
 C;Superfamily: pancreatic secretory trypsin inhibitor; Kazal proteinase inhibitor homolog
 C;Keywords: pancreas; serine proteinase inhibitor
 F;7-56/Domain: Kazal proteinase inhibitor homology <KPI>
 F;9-38,16-35,24-56/Disulfide bonds: #status predicted
 P;18/Inhibitory site: Arg (trypsin) #status predicted

Query Match 84.0%; Score 42; DB 1; Length 56;
 Best Local Similarity 70.0%; Pred. No. 0.21;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCXXIYXPVC 11
 Db 15 GCPRIYNPVC 24

RESULT 4
 TIPG
 pancreatic secretory trypsin inhibitor - pig
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 16-Jul-1999
 C;Accession: A91174; A92079; A90646; A01231
 R;Tschesche, H.; Wachter, E.
 Eur. J. Biochem. 16, 187-198, 1970
 A;Title: The structure of the porcine pancreatic secretory trypsin inhibitor I. A seq
 A;Reference number: A91174; MUID: 70283430; PMID: 5466061
 A;Contents: PSTI I
 A;Accession: A91174
 A;Molecule type: protein
 A;Residues: 1-56 <TSI>
 R;Bartelt, D.C.; Greene, L.J.
 Hoppe-Seyler's Z. Physiol. Chem. 353, 763-764, 1972
 A;Title: Die Disulfidbruecken des Sekretorischen Schweinepankreas-Trypsins
 A;Reference number: A91654; MUID: 73001409; PMID: 4672150
 A;Contents: annotation; disulfide bonds
 R;Tschesche, H.; Wachter, E.
 Hoppe-Seyler's Z. Physiol. Chem. 351, 1449-1459, 1970
 A;Title: Die Primaerstruktur des Spezifischen Trypsininhbitors aus Schweinepankreas
 A;Reference number: A91647; MUID: 71178430; PMID: 5103069
 A;Accession: A92079
 A;Molecule type: protein
 A;Residues: 1-56 <BAR>
 R;Tschesche, H.; Schneider, M.; Reidel, G.; Klein, H.
 Hoppe-Seyler's Z. Physiol. Chem. 353, 763-764, 1972
 A;Title: Die Disulfidbruecken des Sekretorischen Schweinepankreas-Trypsins
 A;Reference number: A91647; MUID: 71178430; PMID: 5103069
 A;Contents: annotation; disulfide bonds
 R;Tschesche, H.; Wachter, E.
 Hoppe-Seyler's Z. Physiol. Chem. 351, 1449-1459, 1970
 A;Title: Die Primaerstruktur des Spezifischen Trypsininhbitors II (Kazal-Typ) aus Schweinepankreas
 A;Reference number: A91647; MUID: 71092915; PMID: 5531651
 A;Contents: PSTI II
 A;Accession: A91647
 A;Molecule type: protein
 A;Residues: 5-56 <TS2>
 R;Manegatti, E.; Bortolotti, F.; Minchiotti, L.; de Marco, A.
 Biochim. Biophys. Acta 707, 50-58, 1982
 A;Title: Isolation and characterization of a new form of the porcine pancreatic secretory trypsin inhibitor
 A;Reference number: A90646; MUID: 83049107; PMID: 7138878
 A;Contents: PSTI III
 A;Accession: A90646
 A;Molecule type: protein
 A;Residues: 9-56 <MEN>
 C;Superfamily: pancreatic secretory trypsin inhibitor; Kazal proteinase inhibitor homolog
 C;Keywords: Pancreas; serine proteinase inhibitor
 F;7-56/Domain: Kazal proteinase inhibitor homology <KPI>
 F;9-38,16-35,24-56/Disulfide bonds: #status experimental
 P;18/Inhibitory site: Lys (trypsin) #status experimental

Query Match 84.0%; Score 42; DB 1; Length 56;
 Best Local Similarity 70.0%; Pred. No. 0.21;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCXXIYXPVC 11
 Db 15 GCPRIYNPVC 24

15 GCPKIYNPVC 24

A;Title: Molecular cloning and characterization of genes encoding rat pancreatic cholecystokinin-releasing peptide; A;Reference number: S28946; MUID:93003324; PMID:1390891
A;Accession: S28946
A;Molecule type: DNA
A;Residues: 1-79 <TS2>
A;Cross-references: DDBJ:D11321; NID:9220694; PID:BA001944.1; R;Uda, K.I.; Ogawa, M.; Shibata, T.; Murata, A.; Mori, T.; Kikuchi, N.; Yoshiida, N.; Tsurugi, K.; Nagata, K.; Yoshida, N.; Tanaka, T.; Yamamoto, M.; Saitoh, Y.; Lett, 191, 269-272, 1985
A;Title: Purification, characterization and amino-acid sequencing of two pancreatic secretin-like peptides; A;Reference number: A01232; MUID:86030679; PMID:4054311
A;Accession: A01232
A;Molecule type: protein
A;Residues: 1-57 <R1K>
A;Keywords: pancreatic secretory trypsin inhibitor; Kazal proteinase inhibitor homolog
A;Domain: Kazal proteinase inhibitor homology <KPI>
A;Disulfide bonds: #status predicted
A;Inhibitory site: Lys (trypsin) #status predicted
A;Score: 42; DB 1; Length 57;
A;Local Similarity 60.0%; Pred. No. 0.21;
A;Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
A;Accession: 178898
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-79 <RES>
A;Cross-references: GB:M35299; NID:9950097; PIDN:AAA74479.1; PMID:9206467
A;Accession: 178898
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 40-76 <RE2>
A;Cross-references: GB:M35300; NID:9206470; PIDN:AAA41977.1; PMID:9206471
C;Comment: This peptide stimulates cholecystokinin release from intestinal mucosal cells
C;Genetics:
A;Gene: PSTI
A;Introns: 19/1; 29/3; 65/2
A;Superfamily: pancreatic secretory trypsin inhibitor; Kazal proteinase inhibitor homolog
C;Keywords: pancreas; serine protease inhibitor
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-79/Product: pancreatic secretory trypsin inhibitor I #status experimental <KPI>
F;30-79/Domain: Kazal proteinase inhibitor homology <KPI>
F;32-61,39-58,47-79/Disulfide bonds: #status predicted
F;41/Inhibitory site: Arg (trypsin) #status predicted
A;Cross-references: EMBL:M22162; NID:9205511; PIDN:AAA41629.1; PMID:9205512
A;Species: Rattus norvegicus (Norway rat)
A;Accession: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jun-2000
A;Reference number: S09602; A33292; A43972; S16223; S28946; S00633; A27111; I58414; I78898
A;Molecule type: mRNA
A;Score: 17, 10111, 1989
A;Title: Complementary nucleotide sequence for monitor peptide, a novel cholecystokinin-releasing peptide; A;Cross-references: S09602; MUID:90098786; PMID:2602119
A;Accession: S09602
A;Molecule type: mRNA
A;Residues: 1-79 <FUK>
A;Cross-references: GB:M27882; NID:9206464; PIDN:AAA41975.1; PMID:9206465
A;Species: S.I.; Scheele, G.A.
A;Accession: A43972
A;Molecule type: mRNA
A;Residues: 1-79 <HOR2>
A;Cross-references: GB:M35299; NID:9950097; PIDN:AAA74479.1; PMID:9206467
A;Species: a cDNA clone with a termination codon following residue 76 was also found
A;Reference number: A43972; MUID:90083122; PMID:2293709
A;Molecule type: mRNA
A;Residues: 1-79 <FU2>
A;Cross-references: GB:M35299; NID:9950097; PIDN:AAA74479.1; PID:9206467
A;Species: a cDNA clone with a termination codon following residue 76 was also found
A;Reference number: A43972; MUID:90083122; PMID:2293709
A;Molecule type: mRNA
A;Residues: 1-79 <TSU>
A;Cross-references: EMBL:X59696; NID:956694; PIDN:CAA42217.1; PMID:956695
A;Note: the authors translated the codon ATA for residue 69 as Met
A;Reference number: S01498; MUID:88111560; PMID:3428272
A;Accession: S01498
A;Molecule type: mRNA
A;Residues: 1-80 <ML>
A;Cross-references: EMBL:X06342; NID:953686; PIDN:CAA29648.1; PMID:953687
A;Note: the authors translated the codon ATA for residue 69 as Met
A;Reference number: S01498; MUID:88111560; PMID:3428272
A;Accession: S01498
A;Molecule type: mRNA
A;Residues: 1-80 <ML>

A;Title: Purification and characterization of a trypsin inhibitor from mouse seminal vesicle
A;Reference number: S18384 ; MUID:92027737 ; PMID:1929395
A;Molecule type: protein
A;Residues: 43-47-49-58-60-61-63-72 <LAI>
C;Comment: The expression of this inhibitor is dependent upon testosterone in prostate
C;Superfamily: pancreatic secretory trypsin inhibitor; Kazal protease inhibitor homology
C;Keywords: pancreas; prostate; seminal vesicle; serine proteinase inhibitor; testis
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-80/Product: pancreatic secretory trypsin inhibitor #status predicted <MAT>
F;31-80/Domain: Kazal proteinase inhibitor homology <KPI>
F;33-62,40-59,48-80/Disulfide bonds: #status predicted
F;42/Inhibitory site: Arg (trypsin) #status predicted

Query Match 84.0%; Score 42; DB 1; Length 80;
Best Local Similarity 70.0%; Pred. No. 0.28; ,
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCXXIXXPVC 11
Db 39 GCPRIYDPVC 48

RESULT 8
A34427 peptide PEC-60 precursor - Pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 17-Feb-1994 #sequence revision 17-Feb-1994 #text_change 16-Jul-1999
C;Accession: A44041; A34427; S24956
R;Metsis, M.; Cintra, A.; Soifer, V.; Ernfors, P.; Bortolotti, F.; Morrasutti, D.G.; Efendi
PROC. Natl. Acad. Sci. U.S.A. 86, 8590-8594, 1989
A;Title: Isolation and characterization of a 60-residue intestinal peptide structurally
A;Reference number: A34427; MUID:90046843 ; PMID:1400298
A;Accession: A44041
A;Molecule type: mRNA
A;Residues: 1-86 <MET>
A;Cross-references: EMBL:X67109; NID:92033; PIDN:CAA47482.1; PID:92034
A;Note: sequence extracted from NCBI backbone (NCBIP:115615)
R;Agerberth, B.; Soederling-Barros, J.; Joernvall, H.; Chen, Z.; Oestenson, C.G.; Efendi
PROC. Natl. Acad. Sci. U.S.A. 86, 8590-8594, 1989
A;Title: Molecular cloning of PEC-60 and expression of its mRNA and peptide in the gastr
A;Reference number: A44041; MUID:93015834 ; PMID:1400298
A;Accession: A44041
A;Molecule type: protein
A;Residues: 1-86 <AGE>
C;Comment: This peptide does not inhibit trypsin. Its biological function is unknown, al
C;Superfamily: pancreatic secretory trypsin inhibitor homology <KPI>
C;Keywords: intestine; leukocyte; serine proteinase inhibitor homology
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-86/Product: peptide PEC-60 #status experimental <MAT>
F;35-86/Domain: Kazal proteinase inhibitor homology <KPI>
F;37-68,46-65/Disulfide bonds: #status Predicted
F;48/Inhibitory site: Arg (unidentified proteinase) #status predicted
F;54-86/Disulfide bonds: #status experimental

Query Match 76.0%; Score 38; DB 1; Length 86;
Best Local Similarity 66.7%; Pred. No. 1.7;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CXXIXXPVC 11
Db 46 CSRIYDPVC 54

RESULT 9
A26730 ovoinhibitor precursor [validated] - chicken
N;Contains: serine proteinase inhibitor (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 01-Sep-2000
C;Accession: A26730
R;Scott, M.J.; Hukaby, C.S.; Kato, I.; Rohr, W.J.; Laskowski Jr., M.; Tsai, M.J.; O'Mall

J. Biol. Chem. 262, 5899-5907, 1987
A;Title: Ovoinhibitor introns specify functional domains as in the related and linked
A;Reference number: A26730 ; MUID:87194792 ; PMID:3571241
A;Accession: A26730
A;Molecule type: mRNA; protein
A;Residues: 1-472 <SCO>
A;Cross-references: GB: M16141; NID:9212483; PIDN:AAA48994.1; PID:9212485
A;Note: parts of this sequence, including the amino end of the mature protein, were d
C;Comment: This is a major inhibitor in blood plasma and also occurs in egg white.
C;Superfamily: chicken ovoinhibitor; Kazal proteinase inhibitor homology
C;Keywords: duplication; egg white; plasma; serine proteinase inhibitor
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-472/Product: ovoinhibitor #status experimental <MAT>
F;26-85/Domain: Kazal proteinase inhibitor homology <KPI1>
F;92-150/Domain: Kazal proteinase inhibitor homology <KPI2>
F;157-216/Domain: Kazal proteinase inhibitor homology <KPI3>
F;223-282/Domain: Kazal proteinase inhibitor homology <KPI4>
F;289-347/Domain: Kazal proteinase inhibitor homology <KPI5>
F;354-413/Domain: Kazal proteinase inhibitor homology <KPI6>
F;420-472/Domain: Kazal proteinase inhibitor homology <KPI7>
F;28-67,45-64,53-85,94-132,110-129,118-150,159-198,176-195,184-216,225-264,242-261,251
F;47/Inhibitory site: Arg (serine proteinase) #status predicted
F;112/Inhibitory site: Arg (serine proteinase) #status predicted
F;178/Inhibitory site: Arg (serine proteinase) #status predicted
F;244/Inhibitory site: Arg (serine proteinase) #status predicted
F;309/Inhibitory site: Phe (serine proteinase) #status predicted
F;375/Inhibitory site: Met (serine proteinase) #status predicted
F;434/Inhibitory site: Met (serine proteinase) #status predicted

Query Match 76.0%; Score 38; DB 1; Length 472;
Best Local Similarity 66.7%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CXXIXXPVC 11
Db 373 CTMIYDPVC 381

RESULT 10
AGR1 agrin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 17-Nov-2000
C;Accession: JH0399; A38856
R;Rupp, F.; Payan, D.G.; Magill-Solc, C.; Cowan, D.M.; Scheller, R.H.
Neuron 6, 811-823, 1991
A;Title: Structure and expression of a rat agrin.
A;Reference number: JH0399; PMID:91222570; PMID:1851019
A;Accession: JH0399
A;Molecule type: mRNA
A;Residues: 1-1779;1799-1959 <RUP>
A;Cross-references: GB: M64780; NID:9202798; PIDN:AAA40703.1; PID:9202800
C;Comment: This protein mediates the motor neuron-induced aggregation of acetylcholine
C;Keywords: agrin; EGF homology; Kazal proteinase inhibitor homology; laminin G re
Y1choline receptor clustering activity.
C;Superfamily: agrin; Kazal proteinase inhibitor homology; neuromuscular junction
C;Keywords: alternative splicing; duplication; glycoprotein; laminin G re
F;1-1959/Product: agrin, form 1 #status predicted <AG1>
F;1-1787,1799-1959/Product: agrin, form 4 #status Predicted <AG4>
F;1-1779,1799-1959/Product: agrin, form 3 #status Predicted <AG3>
F;1-1779,1788-1959/Product: agrin, form 5 #status Predicted <AG5>
F;1-1143,1153-1959/Product: agrin, form 2 #status Predicted <AG2>
F;22-50/Region: hydrophobic

-137/Domain: Kazal proteinase inhibitor homology <KPI1>
 3-212/Domain: Kazal proteinase inhibitor homology <KPI2>
 6-284/Domain: Kazal proteinase inhibitor homology <KPI3>
 7-356/Domain: Kazal proteinase inhibitor homology <KPI4>
 1-429/Domain: Kazal proteinase inhibitor homology <KPI5>
 6-494/Domain: Kazal proteinase inhibitor homology <KPI6>
 1-559/Domain: Kazal proteinase inhibitor homology <KPI7>
 0-542/Region: motor neuron attachment (L-R-E) motif
 16-645/Domain: Kazal proteinase inhibitor homology <KPI8>
 18-739/Domain: laminin-type EGF-like homology <LE1>
 2-786/Domain: laminin-type EGF-like homology <LE2>
 4-864/Domain: Kazal proteinase inhibitor homology <KPI9>
 19-992/Region: serine/threonine-rich
 184-1086/Region: motor neuron attachment (L-R-E) motif
 144-1215/Region: serine/threonine-rich
 124-1257/Domain: EGF homology <EG1>
 187-1442/Domain: laminin G repeat homology <LG1>
 144-1476/Domain: EGF homology <EG2>
 183-1515/Domain: EGF homology <EG3>
 1551206/Domain: laminin G repeat homology <LG2>
 113-1747/Domain: EGF homology <EG4>
 107-1959/Domain: laminin G repeat homology <LG3>
 1-116,105-137,171-191,180-212,244-263,252-284,316-335,324-356,389-408,397-429,454-473
 16,1483-1494,1488-1504,1506-1515/Disulfide bonds: #status predicted
 15,672,827,957/Binding site: carbohydrate (Asn) (covalent) #status predicted
 JLT 11
 138
 nucoid, third domain - Coqui francolin (fragment)
 species: *Francolinus coqui* (*Coqui francolin*)
 date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 07-Feb-1997
 skowski Jr., M.; Kato, I.; Ardel, W.; Cook, J.; Denton, A.; Empie, M.W.; Kohr, W.J.
 ; Wieczorek, M.; Murata, T.; Shibata, T.; Murata, A.; Mori, T.; Kikuchi, N.; Tsur
 chemistry 26, 202-221, 1987
 itie: Ovomucoid third domains from 100 avian species: isolation, sequences, and hyper
 reference number: A90515; PMID:87157615; PMID:3828298
 cession: G31438
 molecule type: protein
 residues: 1-53 <LAS>
 note: the authors designate this sequence with the code OMCOF3
 superfamily: ovomucoid; Kazal proteinase inhibitor homology
 words: egg white; glycoprotein; serine proteinase inhibitor
 53/Domain: Kazal proteinase inhibitor homology <KPI>
 -35-13-32,21-53/Disulfide bonds: #status predicted
 5/Binding site: carbohydrate (Asn) (covalent) #status absent
 2/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
 JLT 12
 340
 tage-gated sodium channel homolog - *Bdelloura candida*
 species: *Bdelloura candida*
 date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 15-Sep-2000
 ccession: T31340
 eitorski, M.C.; Greenberg, R.M.; Anderson, P.A.

submitted to the EMBL Data Library, March 1997
 A;Description: A putative voltage-gated sodium channel from the turbellarian flatworm *Bd*
 A;Reference number: 221006
 A;Accession: T31340
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-1699 <JEZ>
 A;Cross-references: EMBL:U93074; NID:91947093; PID:91947094; PIDN: AAC63049.1
 C;Genetics:
 A;Gene: Na1
 C;Superfamily: sodium channel protein
 Query Match 72.0%; Score 36; DB 2; Length 1699;
 Best Local Similarity 55.6%; Pred. No. 50;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 3 CXXIYXPVC 11
 Db 469 CDDDIYQPC 477
 RESULT 13
 TIR2
 pancreatic secretory trypsin inhibitor II precursor - rat
 N;Alternate names: hepatic proteinase inhibitor
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jun-2000
 C;Accession: B33292; S28947; S08982
 R;Horii, A.; Tomita, N.; Yokouchi, H.; Doi, S.; Uda, K.; Ogawa, M.; Mori, T.; Matsubara,
 Biochem. Biophys. Res. Commun. 162, 151-159, 1989
 A;Title: On the CDNA's for two types of rat pancreatic secretory trypsin inhibitor.
 A;Reference number: A33292; MUID:89322236; PMID:2751646
 A;Accession: B33292
 A;Molecule type: mRNA
 A;Residues: 1-79 <HOR>
 A;Cross-references: GB:M27883
 R;Tsuzuki, S.; Miura, Y.; Fushiki, T.; Oomori, T.; Satoh, T.; Natori, Y.; Sugimoto, E.
 Biochim. Biophys. Acta 1132, 199-202, 1992
 A;Title: Molecular cloning and characterization of genes encoding rat pancreatic cholecyst
 A;Reference number: B33294; MUID:93003324; PMID:1390891
 A;Accession: S28947
 A;Molecule type: DNA
 A;Residues: 1-79 <TSU>
 A;Cross-references: DDBJ:D11325; NID:9220085; PIDN:BAA01945.1; PID:92200887
 R;Uda, K.I.; Ogawa, M.; Shibata, T.; Murata, A.; Mori, T.; Kikuchi, N.; Tsur
 Biol. Chem. Hoppe-Seyler 369(Suppl.), 55-61, 1988
 A;Title: Purification, characterization and amino-acid sequencing of two pancreatic secret
 A;Reference number: S00633; MUID:89076534; PMID:3202973
 A;Accession: S00634
 A;Molecule type: protein
 A;Residues: 24-79 <UDA>
 A;Introns: 19/1; 29/3; 65/2
 C;Superfamily: pancreatic secretory trypsin inhibitor; Kazal proteinase inhibitor homolo
 C;Keywords: pancreas; serine proteinase inhibitor
 F;1-18/Domain: signal sequence #status predicted <SIG>
 F;19-79/Product: pancreatic secretory trypsin inhibitor I #status experimental <MAT>
 F;30-79/Domain: Kazal proteinase inhibitor homology <KPI>
 F;32-61,39-58,47-79/Disulfide bonds: #status predicted
 F;41/Inhibitory site: Arg (trypsin) #status predicted
 Query Match 70.0%; Score 35; DB 1; Length 79;
 Best Local Similarity 60.0%; Pred. No. 61;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 2 GCXXIYXPVC 11

|| | |||
 Db 38 GCPRDYDPVC 47

RESULT 14

JA0128
 hypothetical 11K protein - potato virus S
 C;Species: potato virus S
 A;Note: host Chenopodium quinoa
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
 C;Accession: JA0128
 R;Mackenzie, D.J.; Tremaine, J.H.; Stace-Smith, R.
 J. Gen. Virol. 70, 1063, 1989
 A;Title: Organization and interviral homologies of the 3'-terminal portion of potato virus
 A;Reference number: JA0123; MUID:89279283; PMID:2732711
 A;Accession: JA0128
 A;Molecule type: genomic RNA
 A;Residues: 1-93 <MAC>
 A;Cross-references: GB:D00461; NID:g222438; PIDN:BAA00356.1; PID:92160373
 C;Comment: The genome is a single-stranded, positive-sense RNA.
 C;Superfamily: potato virus nucleic acid-binding protein
 C;Keywords: DNA binding; zinc finger

Query	3 CXXIYXPVC 11	Score 35;	DB 2;	Length 93;
Best Local Similarity	55.6%	Pred. No. 7;		
Matches	5;	Conservative	1;	Mismatches 3; Indels 0; Gaps 0;
Db	57 CYRVYPVPC 65			

RESULT 15

T18525
 diacylglycerol kinase (EC 2.7.1.107) eta - hamster
 N;Alternate names: diglyceride kinase
 C;Species: Cricetinae gen. sp. (hamster)
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
 C;Accession: T18525
 R;Klauck, T.M.; Xu, X.; Mousseau, B.; Jaken, S.
 J. Biol. Chem. 271, 19781-19788, 1996
 A;Title: Cloning and characterization of a glucocorticoid-induced diacylglycerol kinase.
 A;Reference number: Z18948; MUID:96355275; PMID:8702685
 A;Accession: T18525
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-1154 <KLA>
 A;Cross-references: EMBL:U59429; NID:g1401231; PID:g1401232; PIDN: AAC52714.1
 A;Experimental source: strain Syrian
 C;Superfamily: protein kinase C zinc-binding repeat homology
 C;Keywords: phosphotransferase
 F;170-219/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query	3 CXXIYXPVC 11	Score 35;	DB 2;	Length 1154;
Best Local Similarity	55.6%	Pred. No. 57;		
Matches	5;	Conservative	1;	Mismatches 3; Indels 0; Gaps 0;
Db	284 CKDLYHPVC 292			

Search completed: August 11, 2004, 13:09:59
 Job time : 13.0476 secs

GenCore version 5.1.6
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protein - protein search, using SW model
 on: August 11, 2004, 13:01:12 ; Search time 8.38095 Seconds
 (without alignments)
 68.342 Million cell updates/sec

Le: US-10-661-207-2
 Effect score: 50
 Sequence: 1 XGCXXIYXPVC 11

ring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

reched: 141681 seqs, 52070155 residues
 al number of hits satisfying chosen parameters: 141681

imum DB seq length: 0

imum DB seq length: 2000000000

-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

base : SwissProt_42_*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

#	Query	Match	Length	DB	ID	Description
1	4.4	88.0	56	1	IPK1_HORSE	P81634 equus cabal
2	4.4	88.0	79	1	IPK1_HUMAN	P00995 homo sapien
3	4.2	84.0	56	2	IPK1_BOVIN	P00996 bos taurus
4	4.2	84.0	56	1	IPK1_PIG	P00998 sus scrofa
5	4.2	84.0	56	1	IPK1_SHEEP	P00997 ovis aries
6	4.2	84.0	57	1	IPK1_CANFIA	P04542 canis familiaris
7	4.2	84.0	79	1	IPK1_RAT	P09655 rattus norvegicus
8	4.2	84.0	80	1	IPK3_MOUSE	P09036 mus musculus
9	4.0	80.0	69	1	IPK1_STRICA	Q9PBM2 struthio camelus
10	3.9	78.0	197	1	MCP1_MELCP	P82968 melithaea carbonaria
11	3.8	76.0	86	1	ISK4_PIG	P37109 sus scrofa
12	3.8	76.0	156	1	ESM1_DROME	O97176 drosophila melanogaster
13	3.8	76.0	472	1	TOV7_CHICK	P10184 gallus gallus
14	3.8	76.0	1959	1	AGR1_RAT	P25304 rattus norvegicus
15	3.7	74.0	53	1	TOVO_PRACO	P05595 francoalinus
16	3.6	72.0	351	1	DPGN_DIPMA	O96790 dipetalogas
17	3.6	72.0	6684	1	R1AB_CVPPU	Q9iw06 p replicase
18	3.6	72.0	6781	1	R1AB_PEDV7	Q9lav2 p replicase
19	3.5	70.0	79	1	IPK2_RAT	P09656 rattus norvegicus
20	3.5	70.0	93	1	VNBPF_PVSP	P16654 potato virus
21	3.5	70.0	140	1	VNBPF_LSV	P27336 lily symptoma
22	3.5	70.0	1154	1	KDGD_MEASU	Q64398 mesocricetus auratus
23	3.3	66.0	54	1	TOYO_GEOCA	P05615 geococcyx californianus
24	3.2	64.0	223	1	KITH_UREPA	Q9PPPS ureaplasma urealyticum
25	3.2	64.0	806	1	BIMA_EMENI	P17885 emericella
26	3.2	64.0	1955	1	AGR1_CHICK	P31696 gallus gallus
27	31.5	63.0	759	1	PMT6_YEAST	P42934 saccharomyces cerevisiae
28	31	62.0	48	1	IELA_ANESTU	P16895 anemonia sulcata
29	31	62.0	53	1	TOVO_ARBTO	P05601 arborophila
30	31	62.0	53	1	TOVO_FRAAF	P05594 francolinus francolinus
31	31	62.0	56	1	TOVO_FRAER	P34953 macaca fasciata
32	31	62.0	81	1	IAC1_MACFA	P20155 homo sapiens
33	31	62.0	84	1	IAC2_HUMAN	

RESULT 1						
ID	IPK1_HORSE	STANDARD;	PRT;	56 AA.		
AC	P81634;					
DT	15-JUL-1999 (Rel. 38, Created)					
DT	15-JUL-1999 (Rel. 38, Last sequence update)					
DT	10-OCT-2003 (Rel. 42, Last annotation update)					
DE	Pancreatic secretory trypsin inhibitor.					
GN	SPINK1 OR PSTI.					
OS	Equus caballus (Horse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.					
OX	NCBI_TaxID=9796; [1]					
RN	SEQUENCE.					
RP	TISSUE=Pancreas;					
RC	Voit J.;					
RA	"Representation and characterization of pancreatic secretory proteinase inhibitors from various animal species.";					
RA	Ludwig-Maximilians University / Munich, Germany.					
RL	Thesis (1993);					
CC	-!- FUNCTION: This is a trypsin inhibitor, its physiological function is to prevent the trypsin-catalyzed premature activation of zymogens within the pancreas.					
CC	-!- SUBCELLULAR LOCATION: Secreted.					
CC	-!- SIMILARITY: Contains 1 Kazal-like domain.					
DR	HSSP; P37109; 1PCE.					
DR	InterPro; IPR002350; kazal.					
DR	InterPro; IPR001239; kazal_inhib.					
DR	InterPro; IPR00050; kazal; 1.					
DR	pfam; PF00050; kazal.					
DR	PRINTS; PR00290; KAZALINHBTR.					
DR	SMART; SMO0280; KAZAL; 1.					
DR	PROSITE; PS00282; KAZAL; 1.					
KW	Serine protease inhibitor.					
FT	DOMAIN	7	56			
FT	DISULFID	9	38			
FT	DISULFID	16	35			
FT	DISULFID	24	56			
FT	ACT SITE	18	19			
SQ	SEQUENCE	56 AA;	6093 MW;	DODAA7E4FDB507E0 CRC64;		
Query	Match	88.0%	Score 44;	DB 1;	Length 56;	
Best Local	Similarity	70.0%	Pred. No. 0.014;	DB 1;	Length 56;	
Matches	7;	Conservative	0;	Mismatches	3;	Indels 0;
Qy	2 GCXXIYXPVC 11					
Db	15 GCTK1YNPVC 24					

RESULT 2						
ID	IPK1_HUMAN	STANDARD;	PRT;	79 AA.		
AC	P00995;					
DT	21-JUL-1996 (Rel. 01, Created)					
DT	01-MAR-1999 (Rel. 10, Last sequence update)					
DT	10-OCT-2003 (Rel. 42, Last annotation update)					

P58062 homo sapien
 081263 oryza sativa
 P27210 tobacco nec
 P22959 tobacco nec
 Q9i9m5 xenopus laevis
 P59679 brachydanio rerio
 Q9xt49 bos taurus
 P01534 radianthus
 P05617 dacelo novaeguineae
 P05592 cyrtonyx moorii
 P01000 bos taurus
 P41460 autographa californica

ALIGNMENTS

34 31 62.0 85 1 ECG2_HUMAN
 35 31 62.0 212 1 KITH_ORYSA
 36 31 62.0 268 1 COAT_TNVD
 37 31 62.0 276 1 COAT_TNVA
 38 31 62.0 559 1 FZD1_XENLA
 39 31 62.0 623 1 ARP8_BRARE
 40 31 62.0 630 1 S6A4_BOVIN
 41 30 60.0 48 1 TXA2_RADPA
 42 30 60.0 55 1 IOVO_DACNO
 43 30 60.0 56 1 IOVO_CYRMO
 44 30 60.0 63 1 IAC1_BOVIN
 45 30 60.0 84 1 Y056_NPVAC

P58062 homo sapien
 081263 oryza sativa
 P27210 tobacco nec
 P22959 tobacco nec
 Q9i9m5 xenopus laevis
 P59679 brachydanio rerio
 Q9xt49 bos taurus
 P01534 radianthus
 P05617 dacelo novaeguineae
 P05592 cyrtonyx moorii
 P01000 bos taurus
 P41460 autographa californica

Pancreatic secretory trypsin inhibitor precursor (Tumor-associated trypsin inhibitor) (TATI) (Serine protease inhibitor Kazal-type 1). DE MEDLINE=83056875; PubMed=7142173;
 GN RA Huhtala M.-L., Pesonen K., Kalkkinen N., Steinman U.-H.;
 OS RT "Purification and characterization of a tumor-associated trypsin inhibitor from the urine of a patient with ovarian cancer.";
 OC RL J. Biol. Chem. 257:13713-13716 (1982).
 OC RN [8]
 OC X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 OC RX MEDLINE=92309406; PubMed=1613792;
 OC RA Hecht H.-J., Sjöstrand M., Collins J., Schomburg D.;
 OC RA Klaus W., Schomburg D.;
 OC RA "Three-dimensional structure of a recombinant variant of human pancreatic secretory trypsin inhibitor (Kazal type).";
 OC RT J. Mol. Biol. 225:1095-1103 (1992).
 OC RN [9]

SEQUENCE FROM N.A. DE MEDLINE=93164251; PubMed=8433367;
 RX RA Klaus W., Schomburg D.;
 RA "Solution structure of a variant of human pancreatic secretory trypsin inhibitor determined by nuclear magnetic resonance spectroscopy.";
 RA RT J. Mol. Biol. 229:695-706 (1993).
 RN RP VARIANT HPC SER-34, AND VARIANT SER-55.
 RX RA Chen J.-M., Mercier B., Audrezet M.-P., Ferec C.;
 RA RT "Mutation analysis of the human pancreatic secretory trypsin inhibitor (PSTI) gene in hereditary and sporadic chronic pancreatitis.";
 RA RT J. Med. Genet. 37:67-69 (2000).
 CC -!- FUNCTION: This is a trypsin inhibitor, its physiological function is to prevent the trypsin-catalyzed premature activation of zymogens within the pancreas.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DISEASE: Defects in SPINK1 are a cause of hereditary pancreatitis (HPC); also known as chronic pancreatitis (CP). HPC is an autosomal dominant disease characterized by the presence of calculi in pancreatic ducts. It causes severe abdominal pain attacks.
 CC -!- SIMILARITY: Contains 1 Kazal-like domain.

SEQUENCE FROM N.A. DE MEDLINE=20144835; PubMed=10691414;
 RX RA Yamamoto T., Nakamura Y., Nishide T., Emi M., Ogawa M., Mori T., Matsubara K.;
 RA RT "Molecular cloning and nucleotide sequence of human pancreatic secretory trypsin inhibitor (PSTI) cDNA.";
 RL BIochem. Biophys. Res. Commun. 149:635-641 (1987).
 RN RP VARIANT HPC SER-34, AND VARIANT SER-55.
 RX RA Chen J.-M., Mercier B., Audrezet M.-P., Ferec C.;
 RA RT "Mutation analysis of the human pancreatic secretory trypsin inhibitor (PSTI) gene in hereditary and sporadic chronic pancreatitis.";
 RA RT J. Med. Genet. 37:67-69 (2000).
 CC -!- FUNCTION: This is a trypsin inhibitor, its physiological function is to prevent the trypsin-catalyzed premature activation of zymogens within the pancreas.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DISEASE: Defects in SPINK1 are a cause of hereditary pancreatitis (HPC); also known as chronic pancreatitis (CP). HPC is an autosomal dominant disease characterized by the presence of calculi in pancreatic ducts. It causes severe abdominal pain attacks.
 CC -!- SIMILARITY: Contains 1 Kazal-like domain.

SEQUENCE FROM N.A. DE MEDLINE=88083571; PubMed=2961612;
 RX RA Tomita N., Horii A., Yamamoto T., Ogawa M., Mori T., Matsubara K.;
 RA RT "Expression of pancreatic secretory trypsin inhibitor gene in neoplastic tissues.";
 RT PEBS Lett. 225:113-119 (1987).
 RN RP VARIANT HPC PRO-14 AND SER-34, AND VARIANT SER-55.
 RX RA Witt H., Luck W., Hennies H.C., Classen M., Kage A., Lass U., Landt O., Becker M.;
 RA RT "Mutations in the gene encoding the serine protease inhibitor, Kazal type 1 are associated with chronic pancreatitis.";
 RL NAT. Genet. 25:213-216 (2000).
 RN RP VARIANT HPC PRO-14 AND SER-34, AND VARIANT SER-55.
 RX RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Klaunser R.D., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Scheiner A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 99:16899-16903 (2002).
 RN SEQUENCE OF 24-79. DE MEDLINE=77133145; PubMed=843082;
 RX RA Bartelt D.C., Shapanka R., Greene L.J.;
 RT RT "The primary structure of the human pancreatic secretory trypsin inhibitor. Amino acid sequence of the reduced S-aminooethylated protein.";
 RT RL Arch. Biochem. Biophys. 179:189-199 (1977).
 RN SEQUENCE OF 24-46. DE MEDLINE=77133145; PubMed=843082;
 RX RA Bartelt D.C., Shapanka R., Greene L.J.;
 RT RT "The primary structure of the human pancreatic secretory trypsin inhibitor. Amino acid sequence of the reduced S-aminooethylated protein.";
 RT RL Arch. Biochem. Biophys. 179:189-199 (1977).
 RN SEQUENCE OF 24-46.

RX MEDLINE=93164251; PubMed=8433367;
 RA "Pancreatic secretory trypsin inhibitor activity; TAS."
 DR SMART; SM00280; KAZAL; 1.
 DR PROSITE; PS00282; KAZAL; 1.
 KW 3D-structure. FT SIGNAL 1 23
 KW Serine protease inhibitor; Signal; Disease mutation; Polymorphism; FT CHAIN 24 79
 KW DOMAIN 30 79 PANCREATIC SECRETORY TRYPSIN INHIBITOR.
 PT DISULFID 32 61

DISULFID 39 58 REACTIVE BOND.
DISULFID 47 79 L-> P (IN HPC).
ACT SITE 41 42 /FTId=VAR_011688.
VARIANT 14 14 N-> S (IN HPC).
/FTId=VAR_011689.
VARIANT 55 55 P-> S.
/FTId=VAR_011690.
CONFLICT 44 44 D-> N (IN REF. 6 AND 7).
CONFLICT 52 52 N-> D (IN REF. 6).
CONFLICT 64 64 N-> G (IN REF. 3).
SEQUENCE 79 AA; 8507 MW; 3583CB196952EB3A CRC64;
very Match 88.0%; Score 44; DB 1; Length 79;
est Local Similarity 70.0%; Pred. No. 0.02;
atches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Pancreatic secretory trypsin inhibitor.
SPINK1 OR PSTI.
SPINK1 OR PSTI
RN SEQUENCE.
RN MEDLINE=70283430; PubMed=54666061;
RA Tschesche H.; Wachter E.;
RT "The structure of the porcine pancreatic secretory trypsin inhibitor.
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
RN SEQUENCE.
RN MEDLINE=71178430; PubMed=5103069;
RA Bartelt D.C.; Greene L.J.;
RT "The primary structure of the porcine pancreatic secretory trypsin inhibitor. I. Amino acid sequence of the reduced S-aminoethylated protein.";
RT "Sequence determination by Edman degradation and mass spectral identification of the p-bromophenyl-thiohydantoins.";
RT Eur. J. Biochem. 16:187-198 (1970).
RN [1]
RN SEQUENCE.
RN MEDLINE=71178430; PubMed=5103069;
RA Bartelt D.C.; Greene L.J.;
RT "The primary structure of the porcine pancreatic secretory trypsin inhibitor. I. Amino acid sequence of the reduced S-aminoethylated protein.";
RT "Sequence determination by Edman degradation and mass spectral identification of the p-bromophenyl-thiohydantoins.";
RT Eur. J. Biochem. 16:187-198 (1970).
RN [2]
RN SEQUENCE.
RN MEDLINE=73001409; PubMed=4672150;
RA Tschesche H.; Klein H.;
RT "The structure of the porcine pancreatic secretory trypsin inhibitor from procine Kazal's inhibitor. II. The order of the tryptic peptides.";
RT J. Biol. Chem. 244:2646-2657 (1969).
RN SEQUENCE.
RN MEDLINE=72086018; PubMed=5135319;
RA Greene L.J.; Bartelt D.C.;
RT "The structure of the bovine pancreatic secretory trypsin inhibitor -- Kazal's inhibitor. 3. Determination of the disulfide bonds and proteolysis by thermolysin.";
RT J. Biol. Chem. 246:7740-7747 (1971).
RT "-!- FUNCTION: This is a trypsin inhibitor, its physiological function is to prevent the trypsin-catalyzed premature activation of zymogens within the pancreas.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 Kazal-like domain.
PIR; A01230; TIBOA.
HSSP; P37109; 1PCE.
InterPro; IPR002350; kazal.
InterPro; IPR01239; kazal_inhib.
Pfam; PF00050; kazal; 1.
PRINTS; PR00290; KAZAL; 1.
SMART; SM00280; KAZAL; 1.
PROSITE; PS00282; KAZAL; 1.
Serine protease inhibitor.
DOMAIN 7 56 KAZAL-LIKE.
DISULFID 9 38 REACTIVE BOND.
DISULFID 16 35 AB64A512AC851B26 CRC64;
DISULFID 24 56 ACT SITE 18 19 REACTIVE BOND.
SEQUENCE 56 AA; 6161 MW; DR InterPro; IPR002350; kazal.

Query Match 84.0%; Score 42; DB 1; Length 56;
Best Local Similarity 70.0%; Pred. No. 0.036;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCXXIYXPVC 11
Db 15 GCPRIYNPVC 24

RESULT 4
IPK1_PIG STANDARD; PRT; 56 AA.
ID_IPK1_PIG ID_P00998;
AC_P00998; DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pancreatic secretory trypsin inhibitor.
GN SPINK1 OR PSTI.
OS Sus scrofa (Pig).
OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
RN [1]
RN SEQUENCE.
RX MEDLINE=70283430; PubMed=54666061;
RA Tschesche H.; Wachter E.;
RT "The structure of the porcine pancreatic secretory trypsin inhibitor.
I. A sequence determination by Edman degradation and mass spectral identification of the p-bromophenyl-thiohydantoins.";
RT Eur. J. Biochem. 16:187-198 (1970).
RN [2]
RN SEQUENCE.
RX MEDLINE=71178430; PubMed=5103069;
RA Bartelt D.C.; Greene L.J.;
RT "The primary structure of the porcine pancreatic secretory trypsin inhibitor. I. Amino acid sequence of the reduced S-aminoethylated protein.";
RT "Sequence determination by Edman degradation and mass spectral identification of the p-bromophenyl-thiohydantoins.";
RT Eur. J. Biochem. 16:187-198 (1970).
RN [3]
RN SEQUENCE.
RX MEDLINE=71178430; PubMed=5103069;
RA Bartelt D.C.; Greene L.J.;
RT "The primary structure of the porcine pancreatic secretory trypsin inhibitor. I. Amino acid sequence of the reduced S-aminoethylated protein.";
RT "Sequence determination by Edman degradation and mass spectral identification of the p-bromophenyl-thiohydantoins.";
RT Eur. J. Biochem. 16:187-198 (1970).
RN [4]
RN SEQUENCE OF A SECOND INHIBITOR.
RX MEDLINE=73001409; PubMed=4672150;
RA Tschesche H.; Klein H.;
RT "The structure of the porcine pancreatic secretory trypsin inhibitor from procine Kazal's inhibitor. II. The order of the tryptic peptides.";
RT J. Biol. Chem. 244:2646-2657 (1969).
RN SEQUENCE.
RX MEDLINE=83189075; PubMed=7169635;
RA Bolognesi M.; Gatti G.; Menegatti E.; Guarneri M.; Marquart M.;
RA Papamokos E.; Huber R.;
RT "Trypsin inhibitor. VII. Primary structure of the specific trypsin inhibitor II (Kazal-type) from porcine pancreas. Sequence analysis with mass spectrometry identification of the D-bromophenylthio-hydantoins from the Edman degradation.";
RT Hoppe-Seyler's Z. Physiol. Chem. 353:763-764 (1972).
RN [5]
RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RX MEDLINE=83189075; PubMed=7169635;
RA Bolognesi M.; Gatti G.; Menegatti E.; Guarneri M.; Marquart M.;
RA Papamokos E.; Huber R.;
RT "Three-dimensional structure of the complex between pancreatic secretory trypsin inhibitor (Kazal type) and trypsinogen at 1.8-A resolution. Structure solution, crystallographic refinement and preliminary structural interpretation.";
RT J. Mol. Biol. 162:839-868 (1982).
CC -!- FUNCTION: This is a trypsin inhibitor, its physiological function is to prevent the trypsin-catalyzed premature activation of zymogens within the pancreas.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 1 Kazal-like domain.
DR DR PIR; A91174; TIPG.
DR DR PDB; 1TGS; 14-MAR-85.
DR DR InterPro; IPR002350; kazal.

DR InterPro; IPR001239; Kazal_inhib.
 DR Pfam; PF00050; kazal; 1.
 DR PRINTS; PRO0290; KAZALINHBTR.
 DR SMART; SM00280; KAZAL; 1.
 DR PROSITE; PS00282; KAZAL; 1.
 DR Serine protease inhibitor; 3D-structure.
 DOMAIN 7 56 KAZAL-LIKE.
 FT DISULFID 9 38
 FT DISULFID 16 35
 FT DISULFID 24 56 REACTIVE BOND.
 FT ACT SITE 18 19 MISSING (IN A SECOND INHIBITOR).
 FT VARIANT 1 4
 FT STRAND 16 17
 FT STRAND 23 25
 FT TURN 26 27
 FT STRAND 30 31
 FT HELIX 34 42
 FT TURN 43 43
 FT STRAND 50 53
 SQ SEQUENCE 56 AA; 6023 MW; 39A3649DADDF16D25 CRC64;
 Query Match B4.0%; Score 42; DB 1; Length 56;
 Best Local Similarity 70.0%; Pred. No. 0.036;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 RN [1]

Qy 2 GCXXIYXPVC 11
 Db 15 GCPK1YNPVC 24

RESULT 5
 IPK1_SHEEP ID IPK1_SHEEP STANDARD; PRT; 56 AA.
 AC P00957;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Pancreatic secretory trypsin inhibitor.
 GN SPINK1 OR PSTI.
 OS Ovis_aries (Sheep).
 OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae;
 Bovidae; Caprinae; Ovis.
 NCBI_TaxID=9940;
 RN [1]

RP PARTIAL SEQUENCE.
 RA Tschesche H., Obermeier R., Hochstrasser K.;
 RL Unpublished results, cited by:
 RL Tschesche H., Wachter E., Kupfer S., Obermeier R., Reidel G.,
 RL Haenisch G., Schneider M.;
 RL (In) Fritz H., Tschesche H. (eds.);
 RL Proceedings of the international research conference on proteinase
 inhibitors, pp.207-222, Walter de Gruyter, New York (1971).
 CC -!- FUNCTION: This is a trypsin inhibitor, its physiological function
 CC is to prevent the trypsin-catalyzed premature activation of
 CC zymogens within the pancreas.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Contains 1 Kazal-like domain.

Query Match B4.0%; Score 42; DB 1; Length 57;
 Best Local Similarity 60.0%; Pred. No. 0.037;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 RN [1]

Qy 2 GCXXIYXPVC 11
 Db 16 GCNKIYNPIC 25

RESULT 6
 IPK1_CANFA ID IPK1_CANFA STANDARD; PRT; 57 AA.
 AC P04542;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Pancreatic secretory trypsin inhibitor.
 GN SPINK1 OR PSTI.
 OS Canis_familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI_TaxID=9615;
 RN [1]

RP SEQUENCE.
 RX MEDLINE=86030679; PubMed=4054311;
 RA Kikuchi N., Nagata K., Yoshida N., Tanaka T., Yamamoto M., Saitoh Y.;
 RT "Purification and complete amino acid sequence of canine pancreatic
 secretory trypsin inhibitor";
 RL FEBS Lett. 191:269-272 (1985).
 CC -!- FUNCTION: This is a trypsin inhibitor, its physiological function
 CC is to prevent the trypsin-catalyzed premature activation of
 CC zymogens within the pancreas.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MISCELLANEOUS: This Protein is unusual, with respect to the other
 CC mammalian PSTI proteins, in having an extra N-terminal residue.
 CC -!- SIMILARITY: Contains 1 Kazal-like domain.
 DR PIR: A01232; TIDGA.
 DR HSSP; P37109; 1PCE.
 DR InterPro; IPR002350; kazal.
 DR InterPro; IPR001239; Kazal_inhib.
 DR Pfam; PF00050; kazal; 1.
 DR PRINTS; PR00290; KAZALINHBTR.
 DR SMART; SM00280; KAZAL; 1.
 DR PROSITE; PS00282; KAZAL; 1.
 KW Serine protease inhibitor.
 FT DOMAIN 8 57 KAZAL-LIKE.
 FT DISULFID 10 39 BY SIMILARITY.
 FT DISULFID 17 36 BY SIMILARITY.
 FT DISULFID 25 57 BY SIMILARITY.
 FT ACT SITE 19 20 REACTIVE BOND.
 SQ SEQUENCE 57 AA; 6319 MW; 2DE674A2FD98CD43 CRC64;

Query Match B4.0%; Score 42; DB 1; Length 57;
 Best Local Similarity 60.0%; Pred. No. 0.037;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 RN [1]

Qy 2 GCXXIYXPVC 11
 Db 16 GCNKIYNPIC 25

RESULT 7
 IPK1_RAT ID IPK1_RAT STANDARD; PRT; 79 AA.
 AC P09655; P13072;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DE Pancreatic secretory trypsin inhibitor I precursor (PSTI-I).
 DE (Cholecystokinin-releasing peptide) (Monitor peptide).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

SQ SEQUENCE 56 AA; 6145 MW; B8459712AC851B26 CRC64;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;

[1] SEQUENCE FROM N.A.
TISSUE=Pancreas;
MEDLINE=90098786; PubMed=2602119;
Yukoku S.-I., Scheele G.A.;
"Complementary nucleotide sequence for monitor peptide, a novel
cholecystokinin-releasing peptide in the rat.";
Nucleic Acids Res. 17:10111-10111(1989).

[2] SEQUENCE FROM N.A.
STRAIN=Wistar; TISSUE=Pancreas;
MEDLINE=90083122; PubMed=2293709;
Yukoku S.-I., Scheele G.A.;
"Rapid and selective cloning of monitor peptide, a novel
cholecystokinin-releasing peptide, using minimal amino acid sequence
and the polymerase chain reaction.";
Pancreas 5:1-7(1990).

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EMBL; X59696; CAA42217.1; -;
 EMBL; M22162; AAA41629.1; -;
 EMBL; M35299; AAA74479.1; -;
 EMBL; M35300; AAA41977.1; -;
 EMBL; M27882; AAA41975.1; -;
 EMBL; D11321; BAA01944.1; -;
 PIR; S09602; TIBT1;

SMART; SM00280; KAZAL; 1.
PROSITE; PS00282; KAZAL; 1.

Serine protease inhibitor; signal.
SIGNAL 1 18
CHAIN 19 39 PANCREATIC SECRETORY TRYPSIN INHIBITOR I.

KAZAL-LIKE.
BY SIMILARITY.
BY SIMILARITY.

DISULFID ACT SITE 47 41 79 42 BY SIMILARITY. REACTIVE BOND.

CONFLICT /8 /8 1 -> G (IN REF: /) :
SEQUENCE 79 AA; 8528 MW; 5816D55DF7B57874 CRC64;

Very Match 84.0%; Score 42; DB 1; Length 79;
1st Local Similarity 70.0%; Pred. No. 0.05;
1st Score 7; Concentrative 0; Mismatches 3; Index 0;
Gans 0;

2 GCXXIYXPVC 11

38 GCPRIYDPVC 47

Part B
MOUSE

TISK3 MOUSE STANDARD; PRT; 80 AA.
P09036;

01-NOV-1988 (Rel. 09, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)

Serine protease inhibitor Kazar-type 3 precursor (fusobacterial secretory glycoprotein) (P12). SPINK3.

Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.

```
NCBI_TaxID=10090;  
[1] "10090" #>
```

SEQUENCE FROM N.A.
STRAIN=C57BL/6;
MEDLINE=881111560; PubMed=3428272;

Millis J.S., Needham M., Parker M.G.; "A secretory protease inhibitor requires androgens for its expression in male sex accessory tissues but is expressed constitutively in

pancreas." EMBO J. 6:3711-3717 (1987).
PROTECTION. CERTAIN PROTEASE INHIBITORS WHICH EXHIBITS ANTI-TRYPsin

ACTIVITY.
-!- SUBCELLULAR LOCATION: Secreted.

- !- INDUCTION: By androgens.
- !- SIMILARITY: Contains 1 Kazal-like domain.

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CC EMBL; X06342; CAA29648.1; - .
 CC HSSP; P37109; 1PCE.
 CC MGD; MGI:106202; Spink3.
 CC InterPro; IPR0023350; kazal.
 CC InterPro; IPR0012339; kazal_inhib.
 CC PFam; PF00050; kazal; 1.
 CC PRINTS; PR000290; KAZALINHBTR.
 CC SMART; SM00280; KAZAL; 1.
 CC PROSITE; PS00282; KAZAL; 1.
 CC DR SIGNAL 1 23 POTENTIAL.
 CC FT CHAIN 24 80 SERINE PROTEASE INHIBITOR KAZAL-TYPE 3.
 CC FT DOMAIN 31 80 KAZAL-LIKE.
 CC FT DISULFID 33 62 BY SIMILARITY.
 CC FT DISULFID 40 59 BY SIMILARITY.
 CC FT DISULFID 48 80 BY SIMILARITY.
 CC FT ACT SITE 42 43 REACTIVE BOND.
 CC SQ SEQUENCE - 80 AA; 84BB MW; 4DCLF2ECA480CCA6 CRC64;

Query Match Score 42; DB 1; Length 80;
 Best Local Similarity 70.0%; Pred. No. 0.051; 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 3; Del 0; Insert 0; Gapopen 0; Gapclose 0;

Qy 2 GCXXIYXPVC 11
 Db 39 GCPRIYDPVC 48

RESULT 9
 IPK1_STRCA STANDARD PRT; 69 AA.
 ID IPK1_STRCA STANDARD PRT; 69 AA.
 AC Q9PSM2;
 AC DT 16-OCT-2001 (Rel. 40, Created)
 AC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 AC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Pancreatic secretory trypsin inhibitor.
 GN PSTI.
 OS Struthio camelus (Ostrich).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;
 OC Struthio.
 NCBI_TaxID=9801;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=97026357; PubMed=8872536;
 RA Zhao M., Naudé R.J., Muramoto K., Oelofsen W.;
 RT "Purification and characterization of ostrich pancreatic secretory
 trypsin inhibitor.";
 RL Int. J. Pept. Protein Res. 4B:174-181(1996).
 CC "-!- FUNCTION: This is a trypsin inhibitor, its physiological function
 is to prevent the trypsin-catalyzed premature activation of
 zymogens within the pancreas.
 CC "-!- SUBCELLULAR LOCATION: Secreted.
 CC "-!- SIMILARITY: Contains 1 Kazal-like domain.
 DR InterPro; IPR0023350; kazal.
 DR InterPro; IPR0012339; kazal_inhib.
 DR PFam; PF00050; kazal; 1.
 DR PRINTS; PR000290; KAZALINHBTR.
 DR SMART; SM00280; KAZAL; 1.
 DR PROSITE; PS00282; KAZAL; 1.
 KW Serine protease inhibitor.
 CC DOMAIN 12 63 KAZAL-LIKE.
 FT DISULFID 14 45 BY SIMILARITY.
 FT DISULFID 23 42 BY SIMILARITY.
 FT DISULFID 31 63 BY SIMILARITY.
 FT ACT SITE 25 26 REACTIVE BOND.
 SQ SEQUENCE 69 AA; 7656 MW; 199D08A489879579 CRC64;

Query Match Score 39; DB 1; Length 197;
 Best Local Similarity 66.7%; Pred. No. 0.5;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CXXIYXPVC 11

JLT 11
1_PIG _ISK4_PIG STANDARD; PRT; 86 AA.
P37109; 01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Serine protease inhibitor Kazal-type 4 precursor (Peptide PEC-60).
SPINK4.
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suiна; Suidae; Sus.
NCBI_TaxID=9823;

[1]
SEQUENCE FROM N.A.
MEDLINE=93015834; PubMed=1400298;
Agerberth B., Soederling-Barros J., Joernvall H., Bortolotti F.,
Oestenson C.G., Efendic S., Mutt V.;
Norrasutti D.G., Oestenson C.-G., Efendic S., Agerberth B., Mutt V.,
Persson H., Fuxe K.;
"Molecular cloning of PEC-60 and expression of its mRNA and peptide
in the gastrointestinal tract and immune system.";
J. Biol. Chem. 267:19829-19832(1992).

[2]
SEQUENCE OF 27-86.
TISSUE=Intestine;
MEDLINE=90046843; PubMed=2573065;
Agerberth B., Soederling-Barros J., Joernvall H., Chen Z.,
Oestenson C.G., Efendic S., Mutt V.;
"Isolation and characterization of a 60-residue intestinal Peptide
structurally related to the Pancreatic secretory type of trypsin
inhibitor: influence on insulin secretion.";
Proc. Natl. Acad. Sci. U.S.A. 86:8590-8594(1989).

[3]
STRUCTURE BY NMR.
MEDLINE=94254085; PubMed=8196042;
Liepins E., Berndt K.D., Sillard R., Mutt V., Ottung G.;
"Solution structure and dynamics of PEC-60, a protein of the Kazal
type inhibitor family, determined by nuclear magnetic resonance
spectroscopy.";
J. Mol. Biol. 239:137-153(1994).
-!- FUNCTION: Inhibits the glucose-induced insulin secretion from
perfused pancreas; also plays a role in the immune system. Does
not inhibit trypsin.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: SYNTHESIZED IN DUODENAL GOBLT CELLS AND
IN MONOCYTES IN BONE MARROW AND BLOOD.
-!- SIMILARITY: Contains 1 Kazal-like domain.

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or send an email to license@isb-sib.ch).

EMBL; S46866; AB23691.2;-
EMBL; X67109; CAA47482.1;-
PIR; A44041; A34427;
PDB; 1PCE; 30-APR-94.
InterPro; IPR002350; kazal.
InterPro; IPR001239; Kazal_inhib.
Pfam; PF00050; kazal; 1.
PRINTS; PR00290; KAZALINHBTR.
SMART; SM00280; KAZAL; 1.
PROSITE; PS00282; KAZAL; 1.
3D-structure; Signal.
SIGNAL 1 26 SERINE PROTEASE INHIBITOR KAZAL-TYPE 4.
CHAIN 27 86

FT DOMAIN	35	86	KAZAL-LIKE.
FT DISULFID	37	68	
FT DISULFID	46	65	
FT DISULFID	54	86	
FT ACT SITE	48	49	REACTIVE BOND (BY SIMILARITY).
FT TURN	29	30	
FT STRAND	33	33	
FT TURN	41	42	
FT TURN	47	48	
FT STRAND	53	55	
FT TURN	56	57	
FT STRAND	60	61	
FT HELIX	64	74	
FT TURN	75	75	
FT STRAND	80	83	
SQ SEQUENCE	86 AA:	9635 MW;	SD513142CF3A4B4D CRC64;

Query Match	Score 38;	DB 1;	Length 86;
Best Local Similarity	76.0%	pred. No. 0.36;	
Matches 6;	Conservative	0; Mismatches 3;	Indels 0;
Gaps 0;			

Qy 3 CXXIYXPVC 11
Db 46 CSRIYDPVC 54

RESULT 1.2

ESM1_DROME ID	ESM1_DROME	STANDARD;	PRT;	156 AA.
AC O97176;				
DT 16-OCT-2001 (Rel. 40, Created)				
DT 16-OCT-2001 (Rel. 40, Last sequence update)				
DT 10-OCT-2003 (Rel. 42, Last annotation update)				
DE Enhancer of split M1 protein precursor (E(spl) m1).				
GN M1 OR CG8342.				
OS Drosophila melanogaster (Fruit fly).				
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;				
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC Ephydriidae; Drosophilidae; Drosophila.				
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC Ephydriidae; Drosophilidae; Drosophila.				
OX NCBI_TaxID=7227;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC TISSUE=Embryo;				
RX MEDLINE=99173785; PubMed=10072784;				
RA Wurmbach E., Wech I., Preiss A.;				
RT "The Enhancer of split complex of Drosophila melanogaster harbors three classes of Notch responsive genes.";				
RT Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G., Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D.A., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Lai Z.,				
RX STRAIN=Berkeley;				
RX MEDLINE=20196006; PubMed=10731132;				
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G., Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D.A., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Lai Z.,				

RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobaray C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy L., Nixon K., Nusskern D.R., Nelson D.L.,
 RA Nelson D.R., Palazzo M., Pittman G.S., Pan S., Pollard J., Puris M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Rubin J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195 (2000).

-!- DEVELOPMENTAL STAGE: EXPRESSED AT THE TIME WHEN SEPARATION OF
 CC NEURAL AND EPIDERMAL PRECURSORS CELLS OCCURS. ACCUMULATES
 CC TRANSIENTLY AT THE FUSION SITES OF ANTERIOR AND POSTERIOR MIDGUT
 CC AND VERY SPECIFICALLY TO HIGH LEVELS IN THE PROVENTRICULUS OF THE
 CC EMBRYO.

-!- SIMILARITY: Contains 1 Kazal-like domain.

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DR EMBL; AJ010167; CAB39163.1; -.
 DR EMBL; AB003754; AAF56548.1; -.
 DR FlyBase; FBgn0002578; m1.
 DR InterPro; IPR0023350; kazal.
 DR Pfam; PF00050; kazal; 1.
 DR SMART; SM00280; kazal; 2.
 DR PROSITE; PS00282; kazal; FALSE NEG.

KW Serine protease inhibitor; Differentiation; Neurogenesis; Signal.
 FT SIGNAL, 1 19 POTENTIAL.
 FT DOMAIN, 20 156 ENHANCER OF SPLIT M1 PROTEIN.
 SQ SEQUENCE 156 AA; 17339 MW; 5C29F73AE89F6949 CRC64;

Query Match 76.0%; Score 38; DB 1; Length 156;
 Best Local Similarity 66.7%; Pred. No. 0.64;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CXXIXXPVC 11
 DB 106 CSMIYQPVC 114

RESULT 13
 ID IOV7_CHICK STANDARD; PRT; 472 AA.
 AC P10164;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE Ovoinhibitor precursor.
 GN Gallus gallus (Chicken).
 OC Gallinota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;

[1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-472.
 RX MEDLINE=87194792; PubMed=3571241;
 RA Scott M.J., Buckaby C.S., Kato I., Kohr W.J., Laskowski M. Jr.,
 Tsai M.-J., O'Malley B.W.;
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 24-472.

"Ovoinhibitor introns specify functional domains as in the related
 and linked ovomucoid gene.";
 RT RT and linked ovomucoid gene.";
 RL J. Biol. Chem. 262:5899-5907 (1987).
 CC -!- FUNCTION: SEEMS TO HAVE AT LEAST FIVE ACTIVE INHIBITORY DOMAINS;
 CC TWO FOR TRYPSIN, TWO FOR CHYMOTRYPSIN AND ONE FOR ELASTASE.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: EGG WHITE AND PLASMA.
 CC -!- SIMILARITY: Contains 7 Kazal-like domains.
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 CC
 CC DR EMBL; M16141; AAA48994.1; -.
 CC DR EMBL; M15962; AAA48994.1; JOINED.
 CC DR EMBL; M16127; AAA48994.1; JOINED.
 CC DR EMBL; M16128; AAA48994.1; JOINED.
 CC DR EMBL; M16129; AAA48994.1; JOINED.
 CC DR EMBL; M16130; AAA48994.1; JOINED.
 CC DR EMBL; M16131; AAA48994.1; JOINED.
 CC DR EMBL; M16132; AAA48994.1; JOINED.
 CC DR EMBL; M16133; AAA48994.1; JOINED.
 CC DR EMBL; M16134; AAA48994.1; JOINED.
 CC DR EMBL; M16135; AAA48994.1; JOINED.
 CC DR EMBL; M16136; AAA48994.1; JOINED.
 CC DR EMBL; M16137; AAA48994.1; JOINED.
 CC DR EMBL; M16138; AAA48994.1; JOINED.
 CC DR EMBL; M16139; AAA48994.1; JOINED.
 CC DR EMBL; M16140; AAA48994.1; JOINED.
 CC DR PIR; A26730; A26730.
 CC DR HSSP; P055586; 20VO.
 CC DR InterPro; IPR0023350; kazal.
 CC DR InterPro; IPR001239; kazal_inhib.
 CC DR Pfam; PF00050; kazal; 7.
 CC DR PRINTS; PRD0290; KAZALINHBTR.
 CC DR SMART; SM00280; KAZAL; 7.
 CC DR PROSITE; PS00282; KAZAL; 7.
 KW Serine protease inhibitor; Repeat; Signal.
 FT SIGNAL 1 23 OVOINHIBITOR.
 FT CHAIN 24 472
 FT DOMAIN 26 91 KAZAL-LIKE 1.
 FT DOMAIN 92 156 KAZAL-LIKE 2.
 FT DOMAIN 157 222 KAZAL-LIKE 3.
 FT DOMAIN 223 287 KAZAL-LIKE 4.
 FT DOMAIN 288 353 KAZAL-LIKE 5.
 FT DOMAIN 354 419 KAZAL-LIKE 6.
 FT DOMAIN 412 472 KAZAL-LIKE 7.
 FT ACT_SITE 47 48 POSSIBLY TRYPSIN).
 FT ACT_SITE 112 113 REACTIVE BOND 1 (POSSIBLY TRYPSIN).
 FT ACT_SITE 178 179 REACTIVE BOND 2 (POSSIBLY TRYPSIN).
 FT ACT_SITE 244 245 REACTIVE BOND 3 (POSSIBLY TRYPSIN).
 FT ACT_SITE 309 310 REACTIVE BOND 4 (POSSIBLY TRYPSIN).
 FT ACT_SITE 375 376 REACTIVE BOND 5 (POSSIBLY TRYPSIN).
 FT ACT_SITE 375 376 REACTIVE BOND 6 (POSSIBLY TRYPSIN).
 FT ACT_SITE 375 376 REACTIVE BOND 7 (POSSIBLY TRYPSIN).
 FT ACT_SITE 375 376 AND ELASTASE).
 FT DISULFID 28 67
 FT DISULFID 45 64
 FT DISULFID 53 85
 FT DISULFID 94 132
 FT DISULFID 110 129
 FT DISULFID 118 150
 FT DISULFID 159 198
 FT DISULFID 176 195
 FT DISULFID 184 216
 FT DISULFID 225 264
 FT DISULFID 242 261
 FT DISULFID 250 282
 FT DISULFID 291 329

```

DISULFID 307 326
DISULFID 315 347
DISULFID 356 395
DISULFID 373 392
DISULFID 381 413
DISULFID 422 454
DISULFID 432 451
DISULFID 440 472
DISULFID 333 333 MISSING (IN REF. 1; AA SEQUENCE).
SEQUENCE 472 AA: 51919 MW; A30211B29T800E5 CRC64;

every Match    76.0%; Score 38; DB 1; Length 472;
most Local Similarity 66.7%; Pred. No. 1.9;
matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

3 CXXIYXPPVC 11
| | |
373 CTMIYDPVVC 381

JLT 14
:RAT
:AGRI RAT STANDARD; PRT; 1959 AA.
P25304; Q63034;
01-MAY-1992 (Rel. 22, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
NCBI_TAXID=10116;
[1]
SEQUENCE OF 1-1779 AND 1799-1959 FROM N.A.
TISSUE=Embryonic spinal cord;
MEDLINE=91222570; PubMed=1851019;
Rupp F., Payan D.G., Magill-Solc C., Cowan D.M., Scheller R.H. ;
"Structure and expression of a rat agrin.";
Neuron 6:811-823(1991).

[2]
SEQUENCE OF 1777-1801 FROM N.A.
MEDLINE=92407628; PubMed=1326608;
Rupp F., Oezcelik T., Linial M.; Peterson K., Francke U., Scheller R. ;
"Structure and chromosomal localization of the mammalian agrin gene.";
J. Neurosci. 12:3535-3544(1992).
-!- FUNCTION: Component of the basal lamina that causes the
aggregation of acetylcholine receptors and acetylcholine-esterase
on the surface of muscle fibers of the neuromuscular junction.
-!- SUBUNIT: Binds to laminin.
-!- SUBCELLULAR LOCATION: Synaptic basal lamina at the neuromuscular
junction.

-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=5;
Comment=Additional isoforms seem to exist. Isoforms differ in
their acetylcholine receptor clustering activity;
Name=1;
IsoId=P25304-1; Sequence=Displayed;
Name=2;
IsoId=P25304-2; Sequence=VSP_001365;
Name=3;
IsoId=P25304-3; Sequence=VSP_001366;
Name=4;
IsoId=P25304-4; Sequence=VSP_001367;
Name=5;
IsoId=P25304-5; Sequence=VSP_001368;
-!- TISSUE SPECIFICITY: Embryonic nervous system and muscle.
-!- DEVELOPMENTAL STAGE: More abundant early in development.
-!- PTM: Contains heparan sulfate chains as well as N-linked and O-
linked oligosaccharides (By similarity).
-!- SIMILARITY: Contains 9 Kazal-like domains.
-!- SIMILARITY: Contains 2 laminin EGF-like domains.
-!- SIMILARITY: Contains 4 EGF-like domains.

```

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-1- SIMILARITY: Contains 1 SEA domain.
 -1- SIMILARITY: Contains 3 laminin G-like domains.
 -1- CAUTION: It is uncertain whether Met-1, Met-18 or Met-24 is the initiator.

EMBL; M64780; AAA40703_1;
 EMBL; M64780; AAA40702_1; ALT_INIT.
 EMBL; S44194; AAB23326_1;
 PIR; JH0399; AGRT.
 HSSP; P00740; 1EDM.
 InterPro; IPR008985; ConA_like_lec_g1.
 InterPro; IPR006209; EGF_Like.
 InterPro; IPR003645; FOLN.
 InterPro; IPR002350; kazal.
 InterPro; IPR002049; Laminin_EGF.
 InterPro; IPR001791; Laminin_G.
 InterPro; IPR000082; SEA_domain.
 Pfam; PF000008; EGF; 4.
 Pfam; PF00050; kazal; 9.
 Pfam; PF00053; laminin_EGF; 2.
 Pfam; PF00054; laminin_G; 3.
 Pfam; PF01390; SEA; 1.
 PRINTS; PRO0011; EGFLAMININ.
 SMART; SM00180; EGF_Lam; 2.
 SMART; SM00274; FOLN; 8.
 SMART; SM00280; KAZAL; 9.
 SMART; SM00282; LamG; 3.
 SMART; SM00200; SEA; 1.
 PROSITE; PS00022; EGF_1; 6.
 PROSITE; PS01186; EGF_2; 1.
 PROSITE; PS50026; EGF_3; 4.
 PROSITE; PS50025; LAM_G_DOMAIN; 3.
 PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
 PROSITE; PS50024; SEA; 1.
 Glycoprotein; EGF-like domain; Repeat; Alternative splicing; Signal;
 Laminin EGF-like domain; Proteoglycan; Heparan sulfate.
 SIGNAL 1 29
 CHAIN 30 1959
 DOMAIN 65 137
 DOMAIN 141 212
 DOMAIN 213 284
 DOMAIN 287 356
 DOMAIN 361 429
 DOMAIN 430 494
 DOMAIN 495 559
 DOMAIN 563 645
 DOMAIN 688 741
 DOMAIN 742 788
 DOMAIN 794 864
 DOMAIN 1023 1145
 DOMAIN 1220 1258
 DOMAIN 1263 1439
 DOMAIN 1440 1477
 DOMAIN 1479 1516
 DOMAIN 1526 1708
 DOMAIN 1709 1748
 DOMAIN 1784 1956
 DOMAIN 869 992
 DOMAIN 1147 1215
 DISULFID 97 1116
 DISULFID 105 137
 DISULFID 171 191
 DISULFID 180 212
 DISULFID 244 263
 DISULFID 252 284

01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Pancreatic secretory trypsin inhibitor (Fragment).
DE Sub scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydriodea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

[1] RN SEQUENCE FROM N.A.
RP STRAIN=Berkeley;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Abrial J.P., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahake C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong P., Gorrel J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Nixon K., Nusskern D.R., Pacleb J.M., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pollard J., Puri V., Reese M.G., Palazzolo M., Pittman G.S., Pan S., Saunders R.D.C., Scheeler F., Shen H., Reinert K., Remington K., Simpson M., Skupski M.P., Smith T., Shue B.C., Sinden-Kiamos I., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskaus R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; RT "The genome sequence of *Drosophila melanogaster*."; RL Science 287:2185-2195(2000). DR EMBL; AE003600; AAF51914.1; DR FlyBase; FBgn0037405; CG1077. DR GO; GO:0004867; F:serine protease inhibitor activity; IEA. DR InterPro; IPR002350; kazal. DR Pfam; PF000050; kazal; 3. DR SMART; SM00280; KAZAL; 3. DR Sequence 730 AA; 80473 MW; 3290B882D74E5A09 CRC64; KW protease inhibitor; Serine protease inhibitor activity; IEA. DR InterPro; IPR002350; kazal.

Query Match 76.0%; Score 38; DB 5; Length 730; Best Local Similarity 66.7%; Pred. No. 13; Mismatches 0; Indels 3; Gaps 0; Matches 6; Conservative 0; Mismatches 0; Indels 3; Gaps 0; [1] 3 CXXIYXPVC 11 150 CTRIYRPCV 158

RESULT 3 Q29185 PRELIMINARY; PRT; 56 AA.
ID Q29185 DR GO; GO:0005198; F:structural molecule activity; IEA. AC Q29185 DR InterPro; IPRO04850; Agrin_NTA. DT 01-NOV-1996 (TREMBLrel. 01, Created) DR InterPro; IPRO06209; EGF-like. DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update) DR InterPro; IPRO03645; FolN. DR InterPro; IPRO02350; kazal.

[2] RN SEQUENCE OF 1-153 FROM N.A.
RP Groffen A.J.A., Buskens C.A.F., Van Kuppevelt T.H.M.S.M., Veerkamp J.H., Monnens L.A.H., van den Heuvel L.P.W.J.; RA Lennon G., Auffray C., Polymeropoulos M., Soares M.B.; RT "The I.M.A.G.E. Consortium: an integrated molecular analysis of genomes and their expression."; RL Genomics 33:151-152(1996). DR Denzer A.J., Brandenberger R., Gesemann M., Chiquet M., Rueegg M.A. DR EMBL; AF016903; AAC39776.1; -. DR HSSP; P00740; 1EDM. DR Genew; HGNC:329; AGRN. GO; GO:0005198; F:structural molecule activity; IEA. DR InterPro; IPRO04850; Agrin_NTA. DR InterPro; IPRO06209; EGF-like. DR InterPro; IPRO03645; FolN. DR InterPro; IPRO02350; kazal.

[3] RN SEQUENCE OF 1-153 FROM N.A.
RP Denzer A.J., Brandenberger R., Gesemann M., Chiquet M., Rueegg M.A. RL DR EMBL; U84406; AAB52917.1; -. DR HSSP; P00740; 1EDM. DR Genew; HGNC:329; AGRN. GO; GO:0005198; F:structural molecule activity; IEA. DR InterPro; IPRO04850; Agrin_NTA. DR InterPro; IPRO06209; EGF-like. DR InterPro; IPRO03645; FolN. DR InterPro; IPRO02350; kazal.

InterPro; IPR002049; Laminin_EGF.
 InterPro; IPR001791; Laminin_G.
 InterPro; IPR00082; SEA_domain.
 InterPro; IPR00893; TIMP_like.
 InterPro; IPR001455; UPF0033.
 Pfam; PF00008; EGF; 4.
 Pfam; PF00050; kazal; 9.
 Pfam; PF00053; laminin_EGF; 2.
 Pfam; PF00054; laminin_G; 3.
 Pfam; PF03146; Nta; 1.
 Pfam; PF01390; SEA; 1.
 PRINTS; PRO0011; EGFLAMININ.
 SMART; SM00180; EGF_Lam; 2.
 SMART; SM00274; FOLN; 5.
 SMART; SM00280; KAZAL; 9.
 SMART; SM00282; LamG; 3.
 SMART; SM00200; SEA; 1.
 PROSITE; PS00022; EGF_1; 6.
 PROSITE; PS01186; EGF_2; 1.
 PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
 PROSITE; PS50025; LAM_G_DOMAIN; 3.
 PROSITE; PS50024; SEA; 1.
 PROSITE; PS01148; UPF0033; 1.
 EGF-like domain; Laminin_EGF-like domain; Signal.
 NON_TER 1 1
 SIGNAL <1 10 POTENTIAL.
 CHAIN 11 2026 AGRIN.
 SEQUENCE 2026 AA; 212881 MW; 4AB0EE710CD4B8EF CRC64;
 Query Match 74.0%; Score 37; DB 4; Length 2026;
 best Local Similarity 55.6%; Pred. No. 53;
 itches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 CG8369 protein (GH11984p).
 3 CXXIYXPVC 11
 475 CSSLYDPVC 483

JLT 5
 JK7 Q9VHK7 PRELIMINARY; PRT; 94 AA.
 Q9VHK7; 01-MAY-2000 (TREMBLrel. 13, Created)
 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 CG8369 protein (GH11984p).
 /

SEQUENCE FROM N.A.
 STRAIN=Berkeley;
 MEDLINE=20196006; PubMed=10731132;
 Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Guan P., Harris M., Hostin D., Houck J., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K., Nusskern D.R., Pacleb J.M., Reese M.G., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reineert K., Remington K., Saunders R.D.C., Scheuer F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun B., Svartkas R., Tector C., Turner R., Venter S., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zayyeri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., RT "The genome sequence of *Drosophila melanogaster*." Science 287:2185-2195 (2000). [2]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champ M., Dorsett V., Dresneak D., Farfan D., Frise E., Chavez C., Dorsett V., Weissbach J., RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celiker S.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; AE003680; AAPF54297.1; -.
 DR EMBL; AY118777; AAM50637.1; -.
 DR FLYBase; FBgn0040532; CG8369.
 SQ SEQUENCE 94 AA; 10163 MW; 1A8EA3359E5220788 CRC64;

Query Match 72.0%; Score 36; DB 5; Length 94;
 Best Local Similarity 55.6%; Pred. No. 5.2;
 Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

RESULT 6
 Q9VE57 PRELIMINARY; PRT; 145 AA.
 Q9VE57 ID Q9VE57
 AC Q9VE57
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 [1] NCBI_TaxID=7227;
 SEQUENCE FROM N.A.
 STRAIN=Berkeley;
 MEDLINE=20196006; PubMed=10731132;
 Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Guan P., Harris M., Hostin D., Houck J., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K., Nusskern D.R., Pacleb J.M., Reese M.G., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reineert K., Remington K., Saunders R.D.C., Scheuer F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun B., Svartkas R., Tector C., Turner R., Venter S., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zayyeri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., RT "The genome sequence of *Drosophila melanogaster*." Science 287:2185-2195 (2000). [2]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champ M., Dorsett V., Dresneak D., Farfan D., Frise E., Chavez C., Dorsett V., Weissbach J., RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celiker S.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; AE003680; AAPF54297.1; -.
 DR EMBL; AY118777; AAM50637.1; -.
 DR FLYBase; FBgn0040532; CG8369.
 SQ SEQUENCE 94 AA; 10163 MW; 1A8EA3359E5220788 CRC64;

Query Match 72.0%; Score 36; DB 5; Length 94;
 Best Local Similarity 55.6%; Pred. No. 5.2;
 Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Q9VE57 ID Q9VE57
 AC Q9VE57
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 [1] NCBI_TaxID=7227;
 SEQUENCE FROM N.A.
 STRAIN=Berkeley;
 MEDLINE=20196006; PubMed=10731132;
 Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Guan P., Harris M., Hostin D., Houck J., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K., Nusskern D.R., Pacleb J.M., Reese M.G., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reineert K., Remington K., Saunders R.D.C., Scheuer F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun B., Svartkas R., Tector C., Turner R., Venter S., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zayyeri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., RT "The genome sequence of *Drosophila melanogaster*." Science 287:2185-2195 (2000). [2]
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 RL EMBL; AE003680; AAPF54297.1; -.
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Query Match 72.0%; Score 36; DB 5; Length 94;
 Best Local Similarity 55.6%; Pred. No. 5.2;
 Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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 AC Q9VE57
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
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 Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Guan P., Harris M., Hostin D., Houck J., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K., Nusskern D.R., Pacleb J.M., Reese M.G., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reineert K., Remington K., Saunders R.D.C., Scheuer F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun B., Svartkas R., Tector C., Turner R., Venter S., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zayyeri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., RT "The genome sequence of *Drosophila melanogaster*." Science 287:2185-2195 (2000). [2]
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 DR FLYBase; FBgn0040532; CG8369.
 SQ SEQUENCE 94 AA; 10163 MW; 1A8EA3359E5220788 CRC64;

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 STRAIN=Berkeley;
 MEDLINE=20196006; PubMed=10731132;
 Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Guan P., Harris M., Hostin D., Houck J., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K., Nusskern D.R., Pacleb J.M., Reese M.G., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reineert K., Remington K., Saunders R.D.C., Scheuer F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun B., Svartkas R., Tector C., Turner R., Venter S., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zayyeri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., RT "The genome sequence of *Drosophila melanogaster*." Science 287:2185-2195 (2000). [2]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champ M., Dorsett V., Dresneak D., Farfan D., Frise E., Chavez C., Dorsett V., Weissbach J., RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celiker S.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; AE003680; AAPF54297.1; -.
 DR EMBL; AY118777; AAM50637.1; -.
 DR FLYBase; FBgn0040532; CG8369.
 SQ SEQUENCE 94 AA; 10163 MW; 1A8EA3359E5220788 CRC64;

Query Match 72.0%; Score 36; DB 5; Length 94;
 Best Local Similarity 55.6%; Pred. No. 5.2;
 Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Q9VE57 ID Q9VE57
 AC Q9VE57
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 [1] NCBI_TaxID=7227;
 SEQUENCE FROM N.A.
 STRAIN=Berkeley;
 MEDLINE=20196006; PubMed=10731132;
 Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M

RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreria S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Hernandez T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosherfi A., Mount S.M., Moy M., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Yao Q.A., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The Genome sequence of <i>Drosophila melanogaster</i> ."; Science 287:2185-2195 (2000). EMBL; AE003723; AAF55572.1; -.	DR	GO: GO:0006814; P:sodium ion transport; IEA.
RA	FlyBase; FBgn0038631; CG77695.	DR	GO: GO:004867; F:serine protease inhibitor activity; IEA.
RA	InterPro; IPR002350; kazal.	DR	GO: GO:0004867; F:serine protease inhibitor activity; IEA.
RA	SMART; SM00280; KAZAL; 1.	DR	GO: GO:0004867; F:serine protease inhibitor activity; IEA.
KW	Protease inhibitor; Serine protease inhibitor activity; IEA.	DR	GO: GO:0004867; F:serine protease inhibitor activity; IEA.
SQ	SEQUENCE 145 AA; 16581 MW; 4A52F2795CC672B8 CRC64;	DR	GO: GO:0004867; F:serine protease inhibitor activity; IEA.
Query Match	72.0%; Score 36; DB 5; Length 145; Best Local Similarity 66.7%; Pred. No. 7.8; Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	DR	GO: GO:0004867; F:serine protease inhibitor activity; IEA.
Qy	3 CXXIYXPVC 11 95 CPDIYDPVC 103	DR	GO: GO:0004867; F:serine protease inhibitor activity; IEA.
Db	SEQUENCE FROM N.A.	DR	GO: GO:0004867; F:serine protease inhibitor activity; IEA.
RESULT 7	002037 ID 002037 PRELIMINARY; AC 002037; DT 01-JUL-1997 (TREMBLrel. 04, Created) DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update) DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update) DE voltage-gated sodium channel homolog BdDNA1. GN Bdelloura candida. OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida; Maricola; Bdellouriidae; Bdelloura. NCBI_TaxID=46766; RN [1] SEQUENCE FROM N.A. MEDLINE=974455B1; PubMed=9300466; RA Jeziorski M.C., Greenberg R.M., Anderson P.A.V.; RT "Cloning of a putative voltage-gated sodium channel from the turbellarian flatworm <i>Bdelloura candida</i> ."; RT Parasitology 115:289-296 (1997). DR U93074; AAC63049.1; -.	DR	GO: GO:0016021; C:integral to membrane; IEA.
DR	GO: GO:0001518; C:voltage-gated sodium channel complex; IEA.	DR	GO: GO:0005261; F:cation channel activity; IEA.
DR	GO: GO:0005248; F:voltage-gated sodium channel activity; IEA.	DR	GO: GO:0006812; P:cation transport; IEA.
DR	SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RA Kim J.K., Kim Y.H., Lee S.Y.; RL Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases. DR U43905; AAA85904.1; -.	DR	GO: GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR002568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
SEQUENCE 140 AA; 16051 MW; A190FA0BDE82A639 CRC64;

Very Match 70.0%; Score 35; DB 12; Length 140;
est Local Similarity 55.6%; Pred. No. 12;
atches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

3 CXXIYXPVC 11
| :|||
86 CYRVYPVC 94

ULTR 10

Q95P16 PRELIMINARY; PRT; 222 AA.

Q95P16; 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update).
Thrombin inhibitor infestin (Fragment).
Triatoma infestans (Assassin bug).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
Panheteroptera; Cimicomorpha; Reduviidae; Triatomae; Triatoma.
NCBI_TaxID=30076;

[1] SEQUENCE FROM N.A.
TISSUE=anterior midgut; Campos I.T.N., Amino R., Sampiao C.A.M., Auerswald E.A., Friedrich T., Schenkman S., Tanaka A.S.; Lemaire H.-G.; Infestin, a novel thrombin inhibitor present in Triatoma infestans midgut, a Chagas disease vector: cloning, expression and characterization.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

BMBL; AF360846; AAC57342.1; -.
HSSP; P01001; 1BUS.
InterPro; IPR002350; kazal.
InterPro; IPR001239; Kazal_inhib.
PFAM; PF0005290; KAZALINHBTB.

SMART; SM00280; KAZAL; 4.
PROSITE; PS000282; KAZAL; 4.
PROSITE; PS000290; KAZALINHBTB.

PROSITE; PS000290; KAZAL; 4.
SEQUENCE 222 AA; >104 THROMBIN INHIBITOR INFESTIN.
NON_TER 1 1
NON_TER 222 222
SEQUENCE 222 AA; 24370 MW; C9185168B4D41AC3 CRC64;

Very Match 70.0%; Score 35; DB 5; Length 222;
est Local Similarity 55.6%; Pred. No. 18;
atches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

3 CXXIYXPVC 11
| :|||
117 CTKMYKPVC 125

ULTR 11
659 PRELIMINARY; PRT; 385 AA.

Q92659; Q9ILB0; 01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update).
Haptoglobin-related protein.

HPR OR A-259H10.2.
Homo sapiens (Human).
Eukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;

[1]

RP SEQUENCE FROM N.A.
RX MEDLINE=9710114; PubMed=8945641;
RA Tabak S.; Lev A.; Valensi C.; Shalitin C.;
RT "Transcriptionally active haptoglobin-related (hpr) gene in Hepatoma
G2 and leukaemia molt-4 cells;"
RT DNA Cell Biol. 15:1001-1007(1996).
RN [2] RP SEQUENCE OF 40-385 FROM N.A.
RX MEDLINE=9425270; PubMed=10493829;
RA Loftus B.J., Kim U.J., Sneddon V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.L., Mitchell S., Eichler E.S., Harris P.C., Venter J.C., Adams M.D.;
RT "Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";
RL Genomics 60:295-308(1999).
RL !- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC EMBL; X89214; CAA61501.1;
DR DR EMBL; AC004682; AAC27433.1; -.
DR DR HSSP; P08709; 1FAP.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:tryptsin activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys-Ser_trypsin.
DR InterPro; IPR01254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR002922; Pept_S1_HapGnph.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00084; sushi; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYSPC; 1.
DR PROSITE; PS50240; TRYP SIN DOM; 1.
DR PIRSF; PIRSF001137; Haptoglobin; 1.
KW Hydrolase; Protease; Serine protease.
FT VARIANT 376 376 H->D.
SQ SEQUENCE 385 AA; 430777 MW; 8445DD272A496188B CRC64;

Query Match 70.0%; Score 35; DB 4; Length 385;
Best Local Similarity 55.6%; Pred. No. 30;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CXXIYXPVC 11
| :|||
Db 6 CVCVYMPVC 16

RESULT 12
QBF6E2 ID QBF6E2 PRELIMINARY; PRT; 406 AA.
AC QBF6E2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN LA1366.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1] RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovari lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AE011316; AN48565.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 406 AA; 47362 MW;

Query Match 70.0%; Score 35; DB 16; Length 406;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy	2 GCXXIYXPVC 11 : Db 247 GCELYIPSC 256	RESULT 13 Q9LKT8 ID Q9LKT8 PRELIMINARY; PRT; 724 AA. AC Q9LKT8; DT 01-OCT-2000 (TREMBLrel. 15, Created) DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update) DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update) DB Hypothetical protein. GN T32B20.I. OS Arabidopsis thaliana (Mouse-ear cress). OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; OC eurosids II; Brassicales; Brassicaceae; Arabidopsis. OC NCBI_TaxID=3702; RN SEQUENCE FROM N.A. RC STRAIN=cv. Columbia; RA WashU; RT "The A. thaliana Genome Sequencing Project."; RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases. RN [2] RP SEQUENCE FROM N.A. RC STRAIN=cv. Columbia; RA Wilson R.; RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases. DR EMBL; AF262041; AAF67366.1; -. KW Hypothetical protein. SQ SEQUENCE 724 AA; 83057 MW; D75EC74414C20317 CRC64;	RESULT 15 Q7TLU0 ID Q7TLU0 PRELIMINARY; PRT; 82 AA. AC Q7TLU0; DT 01-OCT-2003 (TREMBLrel. 25, Created) DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update) DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update) DE Hypothetical protein. OS Choristoneura fumiferana nuclear polyhedrosis virus (CFMNPV). OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; OC Nucleopolyhedrovirus. OC NCBI_TaxID=208973; RN [1] RP SEQUENCE FROM N.A. RX MEDLINE=93033705; PubMed=1413988; RA Lee H.Y., Arif B., Dobos P., Krell P.; RT "Identification of bent DNA and ARS fragments in the genome of Choristoneura fumiferana nuclear polyhedrosis virus."; RT Virus Res. 24:249-264 (1992). RN [2] RP SEQUENCE FROM N.A. RX MEDLINE=95297142; PubMed=7778276; RA Xie W.D., Arif B., Dobos P., Krell P.J.; RT "Identification and analysis of a putative origin of DNA replication in the Choristoneura fumiferana multinucleocapsid nuclear polyhedrosis virus genome."; RT Virology 209:409-419(1995). RN [3] RP SEQUENCE FROM N.A. RX MEDLINE=95297155; PubMed=7778286; RA Liu J.J., Carstens E.B.; RT "Identification, localization, transcription, and sequence analysis of the Choristoneura fumiferana nuclear polyhedrosis virus DNA polymerase gene."; RT Virology 209:538-549(1995). RN [4] RP SEQUENCE FROM N.A. RX MEDLINE=96030854; PubMed=7595348; RA Barrett J.W., Krell P.J., Ari F.B.M.; RT "Characterization, sequencing and phylogeny of theecdysteroid UDP-glucosyltransferase gene from two distinct nuclear polyhedrosis viruses isolated from Choristoneura fumiferana."; RT J. Gen. Virol. 76:2447-2456(1995). RN [5] RP SEQUENCE FROM N.A. RX MEDLINE=96183379; PubMed=8610448; RA Qiu W., Liu J.J., Carstens E.B.; RT "Studies of Choristoneura fumiferana nuclear polyhedrosis virus gene expression in insect cells."; RT Virology 217:564-572(1996). RN [6] RP SEQUENCE FROM N.A. RX MEDLINE=96400202; PubMed=8806578; RA Liu J.J., Carstens E.B.; RT "Identification, molecular cloning, and transcription analysis of the Choristoneura fumiferana nuclear polyhedrosis virus spindle-like protein gene."; RT Virology 223:396-400(1996). RN [7] RP SEQUENCE FROM N.A. RX MEDLINE=20276145; PubMed=10814576; RA Lapointe R., Back D.W., Ding Q., Carstens E.B.; RT "Identification and molecular characterization of the Choristoneura fumiferana multicapsid nucleopolyhedrovirus genomic region encoding the regulatory genes pkip, p47, lef-12, and gta."; RT Virology 271:109-121(2000). RN [8] RP SEQUENCE FROM N.A. RX MEDLINE=21854555; PubMed=11864738; RA Carstens E.B., Liu J.J., Dominy C.; RT "Identification and molecular characterization of the baculovirus
Qy	2 GCXXIYXPVC 11 : Db 698 GCNAVHIFPMC 707	Query Match Score 35; DB 10; Length 724; Best Local Similarity 40.0%; Pred. No. 54; Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0; RN	2 GCXXIYXPVC 11 : Db 698 GCNAVHIFPMC 707
Qy	2 GCXXIYXPVC 11 : Db 698 GCNAVHIFPMC 707	RESULT 14 Q91GK0 ID Q91GK0 PRELIMINARY; PRT; 82 AA. AC Q91GK0; DT 01-DEC-2001 (TREMBLrel. 19, Created) DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update) DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update) DB Hypothetical protein. OS Epiphyas postvittana nucleopolyhedrovirus. OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; OC Nucleopolyhedrovirus. OC NCBI_TaxID=70600; RN	2 GCXXIYXPVC 11 : Db 698 GCNAVHIFPMC 707
Qy	2 GCXXIYXPVC 11 : Db 82 AA; 9395 MW; 32D80D96EC0324AB CRC64;	SEQUENCE FROM N.A. RA Hyink O., Dellow R.A., Olsen M., Caradoc-Davies K.M.B., Drake K., Ward V.K.; RT "The complete sequence of the Epiphyas postvittana nucleopolyhedrovirus genome."; RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases. DR AY043265; AAK85615.1; -. KW Hypothetical protein. SQ SEQUENCE 82 AA; 9395 MW;	2 GCXXIYXPVC 11 : Db 82 AA; 9395 MW; 32D80D96EC0324AB CRC64;
Qy	3 CXXXIYXPVC 11 : Db 74 CSALLYPLC 826	Query Match Score 34; DB 12; Length 82; Best Local Similarity 44.4%; Pred. No. 12; Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	3 CXXXIYXPVC 11 : Db 74 CSALLYPLC 826

CfMNPV early genes: ie-1, ie-2 and pe38.";
virus Res. 83:13-30(2002).

[9] SEQUENCE FROM N.A.

de Jong J.G., Dominy C.N., Lauzon H.A., Arif B.M., Carstens E.B.,
Krell P.J.;

"Complete Genome of Choristoneura fumiferana Multiple
Nucleopolyhedrovirus.";

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL: AF512031; AAP29838.1; -.

Hypothetical protein.

SEQUENCE 82 AA; 9594 MW; BEBDEEAD779830EF CRC64;

Very Match 68.0%; Score 34; DB 12; Length 82;

1st Local Similarity 44.4%; Pred. No. 12;
Itches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

3 CXXIYXPVC 11
| : | : |
74 CSALYYPLC 82

Search completed: August 11, 2004, 13:09:25
Time : 36.0952 SECs

1ST AVAILABLE COPY